











Qy	757	PCACVLEPCFPYHAGDGFPCASCGG-GLIERPVCC-VEAQSGLKTLFPACCAQAQ	813	Query March	8.54	Score 659.51	DB 2:	Length 2167:
Db	393	ESUSEVCEAEHFGVMECSUTGCGGQGVITVQVYFANGRY-VEDQNYCT--VE	449	Best Local Similarity	24.94	Prod. No. 1.3e-33:		
Qy	814	QPAVALETCNQPCFARNEVSEBSCTAGAGLARETFCVQDGLAPVTEG--PG	870	Matches	239	Conservative 106	Mismatch 379	Indels 237
Db	450	RPVYK-QTQCNFACF-BQAGMSPGKHGDATESGEKAPSPGSGIRTAQAATVPAQ	507					
Qy	871	SVDEKLPAPE--PCVMSGPGKHGDATESGEKAPSPGSGIRTAQAATVPAQ	925					
Db	508	DIQKLPDFTCTCGLGCTVYGENH-----	536					
Qy	926	SCVSGCGRGLMELEKINDSALRVPVQBELGLASGFSRREVCQVPCPARKWQFLAAC	985					
Db	537	-----CGR-----EITRVPVTCDSGR-----ATYLEK	564					
Qy	986	SVSCGGRVREILYCARABEDDBEILLDTCCQGFPPBPQASLE-PPFPMKWS	1044					
Db	565	LN-----LBAVANAASG-----APELCSVT--NEMEAADVICA	797					
Qy	1045	GPCASGLGTAARVAVCQDQGVDEBACALVREASVCLAD-CITRMVOT	1103					
Db	595	SICTEVCGHTRVLCNHLQVGLVVBDSHCQA-REPQKTNCSBKCTGWTSS	653					
Qy	1104	WNCVSCGQDQIRQDQTAQAPVAFQHPVTVVTCGACGQVQGTSPV	1163					
Db	654	WBCVTCGSGQVAVCLN-YDKSEVP-ENCBVAVSEKQCNVDC-----PTCVD	706					
Qy	1164	HEBAAPORT--PCVMSGPGKHGDATESGEKAPSPGSGIRTAQAATVPAQ	1209					
Db	707	SEFQCCPNSTFATGPNFCGSKSEITFGCLNYTVA-----GPNSGGSEVSP	760					
Qy	1210	LBQVTLVYJESU-NCA--GDMLLMGRVTRMCRKLLDMFTSSKTLVPAQ	1265					
Db	761	LN-----LBAVANAASG-----APELCSVT--NEMEAADVICA	797					
Qy	1266	R-----PQGVLYRYSQCAPPTFFRCQDQVPMQVGVSEVSPSPASNAQ--GRL	1316					
Db	798	TIAPITALDQBELIGNDTASNTIH--CSKTEG-----CCDMYTAASGNGSGS	850					
Qy	1317	P 1317						
Db	851	P 851						

Result 7

hypochemical protein C37C3.6b - Caenorhabditis elegans

CSpecies: Caenorhabditis elegans

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

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CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396

CAccession: T34395, T34396



A: Gene: GERP PS186.2

A: Accession: U00260

A: Intron: 38/3; 92/3; 111/3; 126/2; 182/3; 348/2; 376/2; 420/1; 576/3; 759/3; 84

A: Title: Prediction of the coding regions of unidentified human genes. IX. The compl

A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD

A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD

A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD

A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD

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A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD

A: Accession: U00260

A: Title: Preliminary: translated from GB/EWU/DBD





RESULT 14  
 T23061  
 Hypothetical protein T2186.3 - *Caenorhabditis elegans*  
 CSpecies: *Caenorhabditis elegans*  
 CAccession: T23061 #sequenced\_revision 15-Oct-1999 #start\_change 18-Feb-2000  
 R:Kottage, A. Submitted to the EMBL Data Library, November 1995  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 AAccession: T23061 Z1995  
 AMap position: X  
 AIntrons: 20/1; 47/1; 76/1; 152/1; 735/2; 754/2  
 Query March 3, 44; Score 275; DB 2; Length 788;  
 Best Local Similarity 3.44; Pred. No. 1.1e-09; Indels 184; Gaps 28;  
 Matches 112; Conservative 40; Mismatches 149;  
 QY 718 CYSACGACLRWNSYCLDOAKELVETVQCGSPQPPANPEACELECPFPYAVQDFPC 777  
 DB 467 CECTCDGAK-----SRRECTNCGAYE--TEPCLOGCTVWENCMET 514  
 QY 778 SASCGSLGELRPVRVCAQGSLLATIPARCGAQQAQPAVALETCNQPCPT--ARHVESE 835  
 DB 515 SASCGSLGELRPVRVCAQGSLLATIPARCGAQQAQPAVALETCNQPCPT--ARHVESE 835  
 QY 515 SASCGSLGELRPVRVCAQGSLLATIPARCGAQQAQPAVALETCNQPCPT--ARHVESE 835  
 DB 560 WQCVSVCQGVAVPQVPCGLGVPKHLCQPKTE-----QRACQGPCS--W 606  
 QY 893 HLDATACGAESEFMSHIOGAQAHVTPAAGSVSCGRLGMLRFLCDGLALVPVQ 952  
 DB 607 -----SEW-----QWIS-----TCSAGCSQGRP-----A 626  
 QY 953 ELQGLASK--PGRREVCAVCPAPMO--YKLAACSVCGGVVRLLYCARAHG 1007  
 DB 627 QAVCGGTGCGQENESQCTGCP--ANTWENCGSECKSCQGPRTIRPOLGNG 685  
 QY 1008 GEBELLTQCGLPK-----EPOGACS--LECPFPKMGKLPQCSACGLATGERS 1059  
 DB 686 -----ATTQCG--PSLETLCEGCSGKSNBMC-----CNGCQGVYQ 727  
 QY 1060 VACVLDGQGVDEVAQAALVPEASVCLACTAHMG--TWMS--VSCGQIG 1116  
 DB 728 -----IETPFCGENSEPSQLANVQ 752  
 QY 1117 RRDTCLOPAPAPADFOHPLEPVTVRCWAGPVGQGTPLVPEHAAAPRTAT 1176  
 DB 753 SRSACQES-----GC-----KLIC-----LAKESQCCQLTQCP 783  
 QY 1177 PAGA 1181  
 DB 784 KXPC 708  
 RESULT 15  
 brain-specific angiogenesis inhibitor 1 - human  
 NAlternate names: BAI protein  
 CSpecies: *Homo sapiens* (man)  
 CAccession: T23061 #sequenced\_revision 22-Jun-1999 #start\_change 12-Feb-1999  
 R:Nishimori, H.; Shiratuchi, T.; Imano, T.; Kimura, Y.; Miyono, K.; Yonish-Rouss, M.  
 ASubmitted to the EMBL Data Library, June 1997  
 AAccession: T23061 Z14064

A:Status: translated from GB/EMBL/DBJ  
 AAccession: T23061 Z14064  
 AResidues: 1-1584 <HIS>  
 ACross-references: EMBL:AA00297; NID:dt175078; PID:dt024528  
 AExperimental source: Brain  
 CGenetic: BAI  
 AGene: GDB:BAI  
 ACross-references: GDB:1938088; OMIM:602662  
 CSuperfamily: thrombospondin type 1 repeat homology  
 F:438-462/Domain: thrombospondin type 1 repeat homology <THR3>  
 Query March 3, 44; Score 264.5; DB 2; Length 1884;  
 Best Local Similarity 24.04; Pred. No. 1.1e-08; Indels 217; Gaps 43;  
 Matches 164; Conservative 61; Mismatches 242;  
 QY 697 PTFYQPKRQANVAHVRG--PGSVCSAG-LRWNVY-SCIDQAKEL-VETVQ--- 746  
 DB 697 SNTLRNDFERTLWYKAAVPVCS--GGRVITQDFSLFRTYLGESFVRL 135  
 QY 747 -CQCS-----QQP-----AMPEACVLECPFPYAVQDFPC 780  
 DB 136 LQSFALAFQASKQFQWNRQPPQMDQLAPGPGPTDFVYLWQNSPRA 185  
 QY 781 C-----GG-----GLRSEVRCV--EAGSGLIKTPAR--CGAQQA 818  
 DB 186 COMGLDACLASHPQINQTPCCLQSGAGPAGPLA PGVVC--LQVVA 241  
 QY 819 LETCNQPC-----PARNV--SESSCTSAGAGLALENCTVSGADLEAP 864  
 DB 242 ---GFENCLSLTORQDQATGNCMLGMECTHDCQGLQTRTICLP-----AP 292  
 QY 865 VTQSPGVENLPAPEPCVMSGCPGNGHLDATGACBA-----PSP 906  
 DB 293 QVYES--GCQSVLESGQCNHACCPA--GHTSHSGLSGLTARRRBLGDLQGFQFPAP 350  
 QY 907 KGSIRYTAQAHHVTPAAGSVSCGRLGMLRFLCDGLALVPVQ 952  
 DB 351 ---QTDPAEMENSPS--VCSSTCGEQTTRTFVCSVSYVTCQSGPLGRC----- 400  
 QY 962 PGRREVCAVCPAPMO--YKLAACSVCGGVVRLLYCARAHGDDGSEILLTQ 1019  
 DB 401 -NNSAVC--PVRHAEWVPSLCSFTQCGPRTKTRCPPO-----FOGNVKE 447  
 QY 1020 GLVRPEPQ--EASLEPCPCH-----MYVSGFCSAGCTAGRSVACVQDQ--- 1066  
 DB 448 G---PECTKTCNCLQCPGVAVGRHWS--SNSACASCSQCGQTRCNQPSYQ 502  
 QY 1067 -QQQVDEVAQAALVPEASVCLACTV--RMV--GTNMECSQDGTQRRDT 1121  
 DB 503 ECGHNVETRO-----CFQCGVQWQMSAGTQCGPQVQCGQGRREV 546  
 QY 1122 CLGP--QAQAPVAD-----FOHLEPVTVRCWAGPVGQGTPLVPEHAAAPRT 1173  
 DB 549 CSFPFGGACQCPQPTQCTQCTQCTQCTQCTQCTQCTQCTQCTQCTQCTQCT 601  
 QY 1174 TATPAGC---RHLSPGTGIDMGPGQAQVAI-----QDENFGATVKEPVAEVA 601  
 DB 602 VACPRMAGLIGLKEDEBQIAYPEPTTYRC-VSLYANI QWNTHELAQAQGLQ 660  
 QY 1209 ELGEVY-TRVLESSENGAGDM 1231  
 DB 661 GSVSLVQLVETQQDQSYGDL 684

Search completed: March 13, 2004, 07:44:34  
 Job time : 57.425 sec







































FT METAL 405 ZINC (GLUTAMIC) (BY SIMILARITY).

FT CARBOHYD 547 ZINC (GLUTAMIC) (BY SIMILARITY).

FT CARBOHYD 547 N-LINKED (GLNAC. .) (POTENTIAL).

FT CARBOHYD 720 N-LINKED (GLNAC. .) (POTENTIAL).

FT CARBOHYD 782 N-LINKED (GLNAC. .) (POTENTIAL).

FT CARBOHYD 782 N-LINKED (GLNAC. .) (POTENTIAL).

FT CARBOHYD 945 N-LINKED (GLNAC. .) (POTENTIAL).

FT CONFLICT 21 1-2 V (IN REF. 2) (IN REF. 2).

FT CONFLICT 21 1-2 V (IN REF. 2) (IN REF. 2).

FT CONFLICT 49 V -> A (IN REF. 2) (IN REF. 2).

FT CONFLICT 72 R -> P (IN REF. 2).

FT CONFLICT 72 R -> P (IN REF. 2).

FT CONFLICT 79 L -> TR (IN REF. 2).

FT CONFLICT 79 L -> TR (IN REF. 2).

FT CONFLICT 262 TWLA -> NLAK (IN REF. 2).

FT CONFLICT 607 S -> F (IN REF. 2).

FT CONFLICT 607 S -> F (IN REF. 2).

FT CONFLICT 936 L -> V (IN REF. 2).

FT CONFLICT 936 L -> V (IN REF. 2).

FT CONFLICT 945 V -> A (IN REF. 2) (IN REF. 2).

FT SEQUENCE 957 AA; 105705 MW; P93CB64F6DCB4CF CnC64;

Query Match Similarity 12.21; Score 945.5; DB 1; Length 957;

Matches 251; Conservative 111; Mismatches 373; Indels 139; Gaps 30;

QY 4 PTPASHPAPLGLGLALHMGHPHAPCPVPCVGLACPLGCHOPHAPQOCCION 63

DY 177 PAFKESIAAPP-----RFLIRRRR-----GGGACGVVV-----DEETLP 215

DY 64 LEPANVYLFQAKM-----GPPSPGPGQPGQAGAGLLELVANVPVP 216

DY 216 SNGSGESGNTDQGLNFTPGAGTFCG-----SIFKAGSPRYVYLVVAQDQMA 271

DY 117 QACQETRYVYVNIQAEILRPLGQAPRHLVKKVILLTREPAPNTVITSLLS 176

DY 272 DFHSGGLAYLLTYSVAERTKPEIENSISLVYKLVIVYKGVKSPVMAALTUR 331

DY 177 VCGSGTINPDGTHGALVYITREFELPDGROVGTGCGAGSTFWCLITED 236

DY 332 FCSHQKQMSFDQPDYDAILFTPLD-CGSHCTGLGMAVTVCDRESGVIED 390

QY 237 TYPDLQVTTANETGSHGLKQHPG-----SGOCHSHVAV-----DQAPRAQLANSH 287

DY 391 DGLGAFTTAMELGHVFNPDHAKCNKSPVGSUSLHMAISLHNSHP-----NSP 445

QY 288 CSEKQLSELNCGKACWQPPQPGQSGAP-----PDAQGLVYANSCQVAPGAPV 344

DY 446 CSATVYTFNLGNGELCKWKPQ-----NPLKLSQLDPLVDARQCTPFGREETH 498

DY 345 CPTAEKELDQALCHTDPDQSSSELVLLPGLTQSGKQKQKQKQKQKQKQKQK 404

DY 498 CPDA-----ASTSLTACTTGGLGLVQTHFPMADGCEQKQKQKQKQKQKQKQK 555

QY 405 A-VHGSNHPKSPKSCAGQVQVTRPCQNNHPPAPGQVACVGLDQAKMQCQAC-R 462

DY 556 TPTVMSGHPGQGCATQGTQVTRPCQNNHPPAPGQVACVGLDQAKMQCQAC-R 615

QY 463 KXQLENSQCAQCTQGPQ-RESQPGATFTHCAVYACVQKQKQKQKQKQKQKQK 522

DY 616 NGKMTFREQC-EANNEFSHAFKSNPEVTPVTKVAGVSFQDKLTCEANGIOYFVLQ 674

QY 523 DSEFLDTCTHCHSPREDQTLSCVUSCTFGCCQKQKQKQKQKQKQKQKQKQKQK 582

DY 674 PKVYDQVTPCP-----DSY-SVVCQVQKQKQKQKQKQKQKQKQKQKQKQKQK 728

QY 583 QSGTGAQBARVYVTLVPLNLSYLVANLEPLTH-----LAVLIG-QRYVYVGNQSLSP 636

DY 728 QVTSYSTR-QTHDITVTPAGNATVYKGVNFGKSNNGQSFLAIAADQVTLING----- 781

QY 637 NTVVSLPGLERVENVALVEDPLRLEHRLHGPQCADQVQVRYGVRYVYVYVNTDPI 696

DY 781 NPTLSLQK 836

QY 697 TTFYFQPKPQ-----ANV-----MANVGRKVSQCAQLRWVYSLCQAKSLKET 744

DY 837 KYTFKFKCKTEFNPALPTFSRWIEN-----GSKCTGSG-W-----QRVIVEC 881

QY 745 VOQGS-----SQFPAFVACVCEFFVWANGFCGACGQGRVPRVPCVQAG 797

DY 882 RCHNGVASECNEVAPVTPCQALC-FRQVUDASGTPCTGKGVYVPLKLSHSG 940

DY 798 SLKTLFPAKCPAGQAVALETQPCPAP 831

DY 941 GVLSEN-----SSQDLAKPEHY 957

RESULT 13

ID: ATSL MOUSE STANDARD; PRT: 968 AA.

CD PF7857; 054768; 19, Case annotation update

UT 15-OCT-2001 (Ref. 40, Last annotation update)

UT 15-MAR-2004 (Ref. 43, Last annotation update)

DE ADAMTS-1 precursor BC 3.4.24-1 (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS1).

DE ADAMTS-thrombospondin motifs 1

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NBI TaxID:10099.

RM [1]

RP SEQUENCE FROM N.A.

EX MEDLINE=96110583; PUBMED=9441751;

EX MEDLINE=96110583; PUBMED=9441751;

PA Kuno K., Lizaola H., Ohno S., Matsushima K.;

PA "The exon/intron organization and chromosomal mapping of the mouse

PA ADAM family protein with TSP motifs".

PA Genomics 41:465-471(1997).

RP SEQUENCE FROM N.A. PubMed=995297;

PA Kuno K., Kanada N., Nakashima E., Fujiki F., Ichimura F.;

PA Matsushima K.;

PA Molecular cloning of a gene encoding a new type of metalloproteinase-

PA associated protein with a thrombospondin motif as an

PA inflammation associated gene;

PA J. Biol. Chem. 272:565-562(1997).

RP SEQUENCE FROM N.A.

RC TSS2E-Limb, and Mammary gland

RC MEDLINE=2248257; PUBMED=1247932;

PA Kraussers R.L., Costigan P.S., Vagstad R.H., Shinnen C.M., Schuler G.D.,

PA Altschul S.F., Zengbar B., Buetow K.H., Schaefer C.F., Bhat N.K.,

PA Hopkins R.P., Jordan H., Moore T., Max I., Wang J., Hsieh P.,

PA Brownstein M.J., Sances M.B., Bernaldo M., Casavert T.L., Scheetz T.E.,

PA Raha S., Loquellano N.A., Peters G.G., Abramson R.D., Mullaly S.J.,

PA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,

PA Villalon D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,

PA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

PA Blasey A.W., Touchman J.W., Green E.D., Schenck A.C., and G.G.,

PA Blasey A.C., Greenwood J., Schmutz J., Myers R.M.,

PA Butterfield V.S.N., Krywinski M.J., Skolnik U., Smalley D.E.,

PA Genomewide identification of genes expressed in the developing human

PA generation and initial analysis of more than 15,000 full-length

PA human and mouse cDNA sequences;

PA Proc. Natl. Acad. Sci. U.S.A. 99:16999-16993 (2002).

RT CHAOSCATTERIZATION, AND MUTAGENESIS OF GUT-403

RP MEDLINE=99303657; PUBMED=10373500;

PA Kuno K., Terahama Y., Matsushima K.;

PA Extracellular matrix; Metalloproteinases associated with the

PA J. Biol. Chem. 274:18821-18826 (1999).























DB	780	QSEKIBCV	-----KXPFQEEAVJSLCP-----VSTPTVV-----	811
DB	846	GLALNETCVFQAGLEAVPTBQGVQDELPAPFQVQVNSCPFGPHGHDATGAKAP	905	
DB	812	-----CVCNCHAFVPE-----	826	
DB	906	PMGS-RYVQAQHWTPAGCSGCGRLMELFCHMSLRVPEBELGKMGKSR	965	
DB	827	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB	829	-----SQQLTQGVGRVRLV-----KSPAEVLTGSSSPRPS	866	
DB	1026	FOKASLEKFP-----RMVWIAFASGGLTARISACTVQLD-QQGVDEBAC	1078	
DB	867	ADGQALGCFKRNRLGLTANSSNSATLQGVDELKCTKTLQKLTFFBRC	924	
DB	830	-----	838	
DB	837	PA-----	838	
DB	966	REVCAVPCFARMVYKLAQSVQGVVRLYVCAQNGEDDGEHLLDTCCQLPRR	1025	
DB</				







[illegible]





















CC The invention comprises the amino acid and coding sequence of a von  
 CC Willbrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 CC the invention are useful in the diagnosis and treatment of  
 CC von Willebrand disease, thrombotic thrombocytopenic purpura, and  
 CC infectious cerebral infarction, arterioleclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willbrand factor (vWF)-cleaving enzyme-related protein  
 CC  
 CC Sequence 1353 AA;

Query Match 92.8%; Score 1150; DB 6; Length 1353;  
 Match Similarity 91.3%; Oj: Mismatches 0; Indels 34; Gaps 1;  
 Matches 1319; Conservative

Oy 96 AGTILHLELVAVGVGVHAGVGGTETRYVYVNTAGHLEGRVAGVGGVGVVTVIL 157  
 Db 1 AAGTILHLELVAVGVGVHAGVGGTETRYVYVNTAGHLEGRVAGVGGVGVVTVIL 60  
 Oy 158 TETGAPANTVNTAGLSVYGVGGTETRYVYVNTAGHLEGRVAGVGGVGVVTVIL 217  
 Db 61 TETGAPANTVNTAGLSVYGVGGTETRYVYVNTAGHLEGRVAGVGGVGVVTVIL 120  
 Oy 218 VTQGSAGSPFNCCLITETDPTGLVTAHIGUSLEHGVAGVGGVGVVTVIL 277  
 Db 121 VTQGSAGSPFNCCLITETDPTGLVTAHIGUSLEHGVAGVGGVGVVTVIL 180  
 Oy 278 APKALGASPSHGLSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 337  
 Db 181 APKALGASPSHGLSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 240  
 Oy 338 FQPVAVACTFARHLEKQALGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 397  
 Db 241 FQPVAVACTFARHLEKQALGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 300  
 Oy 398 VETPLVAAVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 457  
 Db 301 VETPLVAAVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 360  
 Oy 458 TQACTEQLPFGQCCATGQGLASPGASPGASPGASPGASPGASPGASPGAS 517  
 Db 361 TQACTEQLPFGQCCATGQGLASPGASPGASPGASPGASPGASPGASPGAS 420  
 Oy 518 TMRGSGFLDGLTCHSPREDGLTSLVGSCTGFCVGGVGGVGGVGGVGGVGG 577  
 Db 421 TMRGSGFLDGLTCHSPREDGLTSLVGSCTGFCVGGVGGVGGVGGVGGVGG 480  
 Oy 578 CSPKQSPFAGRAEYVETVLTNLSVYVTAHRLPFLVLAHIGVGVVAGVGG 637  
 Db 540 CSPKQSPFAGRAEYVETVLTNLSVYVTAHRLPFLVLAHIGVGVVAGVGG 540  
 Oy 638 TTVSLDEGRVETVLTEDLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 697  
 Db 541 TTVSLDEGRVETVLTEDLRLRLRLRLRLRLRLRLRLRLRLRLRLRLRL 600  
 Oy 698 FTVFQPKQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 757  
 Db 660 FTVFQPKQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 660  
 Oy 758 EACVLEPQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 817  
 Db 720 EACVLEPQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 720  
 Oy 818 ALFTQPCQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 877  
 Db 780 ALFTQPCQVAAVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 780  
 Oy 878 APKALGASPSHGLSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 937  
 Db 781 APKALGASPSHGLSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSLGSL 840  
 Oy 938 LFTQMSALAVVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 997  
 Db 841 LFTQMSALAVVAVGPGSVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 900

Oy 998 LYCANAGAGDGGDEILLDTQGLPPRPQVACSLCPGPKPKVNGVSPASCLUTAR 1057  
 Db 901 LYCANAGAGDGGDEILLDTQGLPPRPQVACSLCPGPKPKVNGVSPASCLUTAR 960  
 Oy 1058 RSTAVQVQDQ 1117  
 Db 961 RSTAVQVQDQ 1020  
 Oy 1118 RSTAVQVQDQ 1177  
 Db 1021 RSTAVQVQDQ 1080  
 Oy 1178 AG1 AGLASLWEGAGLGLSPAPQGLPPQLPQPNVGGVGGVGGVGGVGG 1203  
 Db 1081 AGLASLWEGAGLGLSPAPQGLPPQLPQPNVGGVGGVGGVGGVGGVGG 1140  
 Oy 1204 VALGPLEVLELVLYVLESLNSACVALLAGVPGVGGVGGVGGVGGVGGVGG 1263  
 Db 1141 VALGPLEVLELVLYVLESLNSACVALLAGVPGVGGVGGVGGVGGVGGVGG 1200  
 Oy 1264 CGPQSGVGLVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 1323  
 Db 1201 CGPQSGVGLVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGGVGG 1260  
 Oy 1324 ARIALVAAVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 1383  
 Db 1261 ARIALVAAVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 1320  
 Oy 1384 LKQASLRSQVLTQVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 1446  
 Db 1321 LKQASLRSQVLTQVHGVSGVSPGSPSCGQVYVTRRQCNTPFAPGECVAGVGLQEN 1353

RESULT 7  
 ID AAO16618 standard; protein; 1997 AA.  
 AC AAO16618;  
 DT 15-MAY-2003 (first entry)  
 DB Human von Willebrand factor (vWF)-cleaving enzyme-related protein #5.  
 KM Human; protease inhibitor; gene therapy; vWF-cleaving enzyme.  
 KM von Willebrand factor; thrombotic thrombocytopenic purpura;  
 KM myocardial infarction; cerebral infarction; arterioleclerosis;  
 KM platelet thrombosis; stenosis.  
 XX Homo sapiens.  
 XX MO20028366-A1.  
 PU 07-NOV-2002.  
 PP 25-APR-2002; 2002NC-JP004141.  
 PP 25-APR-2001; 2001JP-00128342.  
 PR 27-JUL-2001; 2001JP-0027510.  
 PR 28-SEP-2001; 2001JP-00303977.  
 PR 25-JAN-2002; 2002JP-00017596.  
 PA (KAGA) CHMO-SERO-THEAPEUTIC RES INF.  
 PA Soejima K, Miumura N, Mieda H, Noraki C, Hamamoto T, Nakagaki T;  
 DR MP1; 2003-120479/11.  
 DR N-PSDB; AP325584.  
 DR von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 DR supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
 DR developing drugs for e.g. myocardial infarction and cerebral infarction.  
 XX







von Willebrand factor-clawing enzyme, and for  
supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
developing drugs for e.g. myocardial infarction and cerebral infarction.

Claim 4; Page 112-121; 144pp; Japanese.

The invention comprises the amino acid and coding sequence of a von  
Willebrand factor-clawing enzyme, and the invention also comprises sequences of  
the invention are useful in the diagnosis and treatment of myocardial  
thrombotic purpura, and in developing drugs for myocardial  
infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
thrombotic thrombocytopenic purpura, and for developing drugs for a human von  
Willebrand factor (vWF)-clawing enzyme-related protein

Sequence 123 AA;

Query Match: 87.18; Score 6752.5; DB 6; Length 1323;

Best Local Similarity 93.18; Pred. No. 0;

Matches 1257; Conservative 4; Mismatches 33; Indels 53; Gaps 5;

98 AAGCILLVLAVGVDFQAFQAEQRTVTLNLTGAEILRPLGACPLVHLVNVIL 157

1 AAGCILLVLAVGVDFQAFQAEQRTVTLNLTGAEILRPLGACPLVHLVNVIL 60

158 TEPGAPNTANTSLVSCMSQNTINPEDDTDHADVILITFPLEDQFNQVWG 217

61 TEPGAPNTANTSLVSCMSQNTINPEDDTDHADVILITFPLEDQFNQVWG 120

218 VTQGLGACFPNLSCLITEDTQDVLGTIAHLSHSGHLEADVAGSCPSRMASSGA 277

121 VTQGLGACFPNLSCLITEDTQDVLGTIAHLSHSGHLEADVAGSCPSRMASSGA 180

278 APRAGIANSPCKRALLSLASG-----RARCWDPR 310

181 APRAGIANSPCKRALLSLASG-----RARCWDPR 240

311 PQSGAGHPEDAGPQLYSARQVAF-GPKAVACTFARELLQCALSCITDPLGSS 369

241 PQ-CHCLLHAGQAP--ESAGGGLGAVRSURITQUTSPQTDGACQALSCITDPLGSS 297

370 CSELVPLLDGTCVETKNSGKGRCSLVELTPIAAVHGSNGSPKSPCSRGQVVT 429

298 CSELVPLLDGTCVETKNSGKGRCSLVELTPIAAVHGSNGSPKSPCSRGQVVT 357

430 CSELVPLLDGTCVETKNSGKGRCSLVELTPIAAVHGSNGSPKSPCSRGQVVT 489

358 RRCQNRAPAGACVADQENQCNQACNTQACNTQENQCNQACNTQACNTQACNTQACNT 417

490 FTHGAVPHQGDALCRKCAIGESFIMGDSQFTDGTGNGRSDTLGICVSS 549

418 FTHGAVPHQGDALCRKCAIGESFIMGDSQFTDGTGNGRSDTLGICVSS 477

550 CRTGCGRMGSCQMDRCQVQNDGNTSCPRGSGFAGAREVITLITPLTGVTA 609

478 CRTGCGRMGSCQMDRCQVQNDGNTSCPRGSGFAGAREVITLITPLTGVTA 537

610 NHRPLFLALVGTIVAGNLSINTPTTLLBDRVTRVALTERLURLEITLM 669

538 NHRPLFLALVGTIVAGNLSINTPTTLLBDRVTRVALTERLURLEITLM 597

720 GPLDEADQVTERGEYQNTTPTLTITFPPKPMQMAVAGPSCSQCAGLWY 729

596 GPLDEADQVTERGEYQNTTPTLTITFPPKPMQMAVAGPSCSQCAGLWY 657

730 NYSCLQAKSELVELTCCGSGPAMPACVLECFPTPAVAGPDCSACQGLRFP 789

658 NYSCLQAKSELVELTCCGSGPAMPACVLECFPTPAVAGPDCSACQGLRFP 717

790 VRCVCGSLKLTLPACRAGAQVALETQPCFAPMEVESECTSGAGLAL 849

718 VRCVCGSLKLTLPACRAGAQVALETQPCFAPMEVESECTSGAGLAL 777

850 ENETCVPGAGLEAVTFEPGQVSEKLPAPFCVMSQFPGHGLMATEAFSPWG 909

778 ENETCVPGAGLEAVTFEPGQVSEKLPAPFCVMSQFPGHGLMATEAFSPWG 937

910 IRTGQANWPTPAGSCVSCGCRGKLEFLVQNSALVTPVQELGLASFGSGREVC 969

838 IRTGQANWPTPAGSCVSCGCRGKLEFLVQNSALVTPVQELGLASFGSGREVC 897

970 QAVCPASRWQYVCLAGVQCVRELLVLCVHSGEDGDEELLLTQCGLPREPQEA 1029

898 QAVCPASRWQYVCLAGVQCVRELLVLCVHSGEDGDEELLLTQCGLPREPQEA 957

1030 GSELPCEPRKYNKLGSCASCLGTATREAVYVQLQDQGVVEBACALVPEASVP 1089

958 GSELPCEPRKYNKLGSCASCLGTATREAVYVQLQDQGVVEBACALVPEASVP 1017

1090 CLANCTVRRVDTNMEVSCDCGQIRREDDTLGPAQAPVAFQHLPPVTVGWC 1149

1018 CLANCTVRRVDTNMEVSCDCGQIRREDDTLGPAQAPVAFQHLPPVTVGWC 1077

1150 AGSCVQGGTSLVPREAAAGRTTAPAGACGQLEFPTQIMRGPGGACAVAGRP 1209

1078 AGSCVQGGTSLVPREAAAGRTTAPAGACGQLEFPTQIMRGPGGACAVAGRP 1115

1210 LGSEVTVLRVBSLNSGCMGLLWGLTRKMLDMLTFSSTNLVVRQCRFG 1269

1116 LGSEVTVLRVBSLNSGCMGLLWGLTRKMLDMLTFSSTNLVVRQCRFG 1175

1270 GVLYESGLASDETFTECDQCPKGEVSESLSPASNAQCLPFINAPARIAIN 1329

1176 GVLYESGLASDETFTECDQCPKGEVSESLSPASNAQCLPFINAPARIAIN 1235

1330 ALATNGAGTEGANNSTILLRDTHELTTAFHQOVLMESSQMSSEFSDFLKAQS 1389

1236 ALATNGAGTEGANNSTILLRDTHELTTAFHQOVLMESSQMSSEFSDFLKAQS 1295

1390 LGQWTQLQSWPBMQDPSQMKDET 1416

1296 LGQWTQLQSWPBMQDPSQMKDET 1322

RESULT 10

AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

XX AAU792121 standard; protein: 933 AA.

DR WPI: 2002-383274/1.  
 XX N-PDB: A84356.  
 XX New purified human ADM-7S-like protein, useful for identifying  
 XX modulators of protein activity for treating cardiovascular or liver  
 XX disorder or chronic obstructive pulmonary disease.  
 XX Claim 25; Fig 2; 10pp; English.  
 XX  
 XX The invention relates to a human ADM-7S-like protein and the  
 XX polypeptide sequences and disorders including diseases of the heart and  
 XX vascular system, such as congestive heart failure, myocardial infarction,  
 XX ischemic heart diseases (e.g., stable angina, unstable angina), atrial  
 XX fibrillation, and peripheral vascular diseases, and peripheral vascular  
 XX kinds of secondary arterial hypertension, and peripheral vascular  
 XX diseases (e.g., chronic peripheral arterial occlusive disease, acute  
 XX arterial thrombosis and embolism, inflammatory vascular disorders, aco),  
 XX and other diseases of the heart and vascular system. The protein and  
 XX are useful in diagnostic assays for detecting diseases and abnormalities  
 XX or susceptibility to diseases and abnormalities related to the presence  
 XX of mutations in the nucleic acid sequences which encode the protein. In  
 XX addition, the protein and nucleic acid sequences are useful in the treatment  
 XX of a disease condition. This sequence represents the human ADM-7S-like  
 XX protein.  
 XX  
 XX Sequence 933 AA;  
 XX  
 XX Query Match 57.2%; Score 4434.5; DB 5; Length 933;  
 XX Best Local Similarity 91.6%; Pred. No. 0;  
 XX Matches 81%; Conservative 42; Aminoacids 8; Indels 65; Gaps 3;  
 XX  
 XX 64 LEP-----QAVSSTLSPALKPSFQFQQRQRQRRAAGIHLHLVAVGVDFVAA 119  
 XX 41 LEPGLKATLALCSHPP-PSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 99  
 XX 120 QDTERVYVNLNLCALLRDSNGQFVHLVWVLTPEPAPNTATITSSLSSTG 179  
 XX 100 QDTERVYVNLNLCALLRDSNGQFVHLVWVLTPEPAPNTATITSSLSSTG 159  
 XX 180 WQTIHPEDTRGALVLTITFELPQGRVQVGTQGLQCSPTFNCILTEDTP 239  
 XX 160 WQTIHPEDTRGALVLTITFELPQGRVQVGTQGLQCSPTFNCILTEDTP 219  
 XX 240 DLTGTATETGHEFLRHDQGGQSGHSHWQDAFAGLAWSPSCROLLSLSH 299  
 XX 220 DLTGTATETGHEFLRHDQGGQSGHSHWQDAFAGLAWSPSCROLLSLSH 279  
 XX 300 GRACWQWPPRQPSGSHDQGLYLSNQRVACTFASHLWQGLS 359  
 XX 280 GRACWQWPPRQPSGSHDQGLYLSNQRVACTFASHLWQGLS 339  
 XX 360 CHTPDLQSSGSHLLVLTGQTEVMSKGRCSKLVETLTAHVRMSQPRFC 419  
 XX 340 CHTPDLQSSGSHLLVLTGQTEVMSKGRCSKLVETLTAHVRMSQPRFC 399  
 XX 420 RSGSGVYVTRQGNPPFAFGACVACALANVQALTEFLPMQSGQCTG 479  
 XX 400 RSGSGVYVTRQGNPPFAFGACVACALANVQALTEFLPMQSGQCTG 459  
 XX 480 FLSSFGGAFTHVAVHSGALCHNCALBELTQVMSQSDTQVMSQSDTQV 539  
 XX 460 FLSSFGGAFTHVAVHSGALCHNCALBELTQVMSQSDTQVMSQSDTQV 519  
 XX 540 QTLSSGSHCTCGDMSQWQWQWQWQWQWQWQWQWQWQWQWQWQWQW 599  
 XX 520 QTLSSGSHCTCGDMSQWQWQWQWQWQWQWQWQWQWQWQWQWQWQW 579  
 XX 600 TPAVAVVAVNBAVAVNBAVAVNBAVAVNBAVAVNBAVAVNBAVAVN 659  
 XX 580 TPAVAVVAVNBAVAVNBAVAVNBAVAVNBAVAVNBAVAVNBAVAVN 639  
 XX 660 LPELEIRNGPLADADICQVKVIGSSASLADPPVGLKLVNTGTGLEHWDV 699  
 XX 679 -----QVHRYEYVNGTDPITTFYFQKQVMAVWVQFCS 719  
 XX 700 TEGAQVSNCTPGLSPGVYHRYEYVNGTDPITTFYFQKQVMAVWVQFCS 759  
 XX 720 VSGAGLWNVNSCLQKRLVETVQSGSPANFPAVCTVETCFYVWQDFCSA 779  
 XX 760 VSGAGLWNVNSCLQKRLVETVQSGSPANFPAVCTVETCFYVWQDFCSA 819  
 XX 780 SCGGGLERPVCTEYAGSLKLTLPACBAQAPVALTCTQPCFARVSEFSC 839  
 XX 820 SCGGGLERPVCTEYAGSLKLTLPACBAQAPVALTCTQPCFARVSEFSC 879  
 XX 840 TSAGAGLALNETHVCTPADGLAEVTEGTVDEKLPAPFCVQSGPPQWH 893  
 XX 880 TSAGAGLALNETHVCTPADGLAEVTEGTVDEKLPAPFCVQSGPPQWH 933  
 XX  
 XX RESULT 11  
 XX AD636352 standard; protein, 1120 AA.  
 XX XN: AAG63829 standard; protein, 1120 AA.  
 XX AC AAG63829;  
 XX AD: 29-OCT-2001 (first entry)  
 XX  
 XX XN: Amino acid sequence of a human zdnt5 polypeptide.  
 XX XN: Human; zdnt5; anti-angiogenic; intestinal polypeptide; wound healing;  
 XX XN: extracellular matrix interaction; tumor suppression; gamete maturation;  
 XX XN: immunologic recognition; gastrointestinal irradiation; tumor adhesion;  
 XX XN: cell fusion; cell signaling; tumor; Crohn's disease; melanoma; trauma;  
 XX XN: inflammatory bowel disease; food poisoning; degenerative disease;  
 XX XN: inflammation; fertility; gamete maturation; epithelial disorder.  
 XX XN: Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Modified-site /note= "potential N-linked glycosylation site"  
 XX Modified-site 176 /note= "potential N-linked glycosylation site"  
 XX Misc-difference /note= "unspecified residue encoded by TTN"  
 XX Modified-site 495 /note= "potential N-linked glycosylation site"  
 XX Modified-site 533 /note= "potential N-linked glycosylation site"  
 XX Modified-site 560 /note= "potential N-linked glycosylation site"  
 XX Modified-site 595 /note= "potential N-linked glycosylation site"  
 XX Modified-site /note= "potential N-linked glycosylation site"  
 XX Modified-site 635 /note= "potential N-linked glycosylation site"  
 XX W0201159112-1.  
 XX  
 XX 16-AUG-2001.  
 XX  
 XX 09-FEB-2001; 2001NC-US004198.  
 XX 10-FEB-2000; 2000US-00501806.  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX Holloway JL, Sheppard PO.  
 XX WPI: 2001-52477/57.  
 XX N-PDB: A487165.  
 XX



[illegible]

Qy 8 KAPSHSAPLLGLALLRMHQHPRARCPPLCVAGILACGFLGCGWPSHFQSCIQALEPQ 67

1132	PADFQHLPEKVTYVRCWAGCGVQCTPSLPVHEEAAAGRTTATAGACGRLFTGT	1151	.....	1170	.....	1189	.....	1208	.....	1227	.....	1246	.....	1265	.....	1284	.....	1303	.....	1322	.....	1341	.....	1360	.....	1379	.....	1398	.....	1417	.....	1436	.....	1455	.....	1474	.....	1493	.....	1512	.....	1531	.....	1550	.....	1569	.....	1588	.....	1607	.....	1626	.....	1645	.....	1664	.....	1683	.....	1702	.....	1721	.....	1740	.....	1759	.....	1778	.....	1797	.....	1816	.....	1835	.....	1854	.....	1873	.....	1892	.....	1911	.....	1930	.....	1949	.....	1968	.....	1987	.....	2006	.....	2025	.....	2044	.....	2063	.....	2082	.....	2101	.....	2120	.....	2139	.....	2158	.....	2177	.....	2196	.....	2215	.....	2234	.....	2253	.....	2272	.....	2291	.....	2310	.....	2329	.....	2348	.....	2367	.....	2386	.....	2405	.....	2424	.....	2443	.....	2462	.....	2481	.....	2500	.....	2519	.....	2538	.....	2557	.....	2576	.....	2595	.....	2614	.....	2633	.....	2652	.....	2671	.....	2690	.....	2709	.....	2728	.....	2747	.....	2766	.....	2785	.....	2804	.....	2823	.....	2842	.....	2861	.....	2880	.....	2899	.....	2918	.....	2937	.....	2956	.....	2975	.....	2994	.....	3013	.....	3032	.....	3051	.....	3070	.....	3089	.....	3108	.....	3127	.....	3146	.....	3165	.....	3184	.....	3203	.....	3222	.....	3241	.....	3260	.....	3279	.....	3298	.....	3317	.....	3336	.....	3355	.....	3374	.....	3393	.....	3412	.....	3431	.....	3450	.....	3469	.....	3488	.....	3507	.....	3526	.....	3545	.....	3564	.....	3583	.....	3602	.....	3621	.....	3640	.....	3659	.....	3678	.....	3697	.....	3716	.....	3735	.....	3754	.....	3773	.....	3792	.....	3811	.....	3830	.....	3849	.....	3868	.....	3887	.....	3906	.....	3925	.....	3944	.....	3963	.....	3982	.....	4001	.....	4020	.....	4039	.....	4058	.....	4077	.....	4096	.....	4115	.....	4134	.....	4153	.....	4172	.....	4191	.....	4210	.....	4229	.....	4248	.....	4267	.....	4286	.....	4305	.....	4324	.....	4343	.....	4362	.....	4381	.....	4400	.....	4419	.....	4438	.....	4457	.....	4476	.....	4495	.....	4514	.....	4533	.....	4552	.....	4571	.....	4590	.....	4609	.....	4628	.....	4647	.....	4666	.....	4685	.....	4704	.....	4723	.....	4742	.....	4761	.....	4780	.....	4799	.....	4818	.....	4837	.....	4856	.....	4875	.....	4894	.....	4913	.....	4932	.....	4951	.....	4970	.....	4989	.....	5008	.....	5027	.....	5046	.....	5065	.....	5084	.....	5103	.....	5122	.....	5141	.....	5160	.....	5179	.....	5198	.....	5217	.....	5236	.....	5255	.....	5274	.....	5293	.....	5312	.....	5331	.....	5350	.....	5369	.....	5388	.....	5407	.....	5426	.....	5445	.....	5464	.....	5483	.....	5502	.....	5521	.....	5540	.....	5559	.....	5578	.....	5597	.....	5616	.....	5635	.....	5654	.....	5673	.....	5692	.....	5711	.....	5730	.....	5749	.....	5768	.....	5787	.....	5806	.....	5825	.....	5844	.....	5863	.....	5882	.....	5901	.....	5920	.....	5939	.....	5958	.....	5977	.....	5996	.....	6015	.....	6034	.....	6053	.....	6072	.....	6091	.....	6110	.....	6129	.....	6148	.....	6167	.....	6186	.....	6205	.....	6224	.....	6243	.....	6262
------	---	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------	-------	------

28-NOV-2001; 2001US-0333891P.  
PR PI Ralinger SK, Altman K, Gangoli EA, Gurevich CE, Casman SJ;  
PI Gunter E, Herrmann JL, Ji W, Lepley DM, Lewin DA, Li J;  
PI Macdonald AS, Malyukova DN, Mezes PD, Padigam N, Shetty S,  
PI Sathyanarayana SG, Schmitt KA, Taugler AJ, Thernberg Vt;  
PI Satishan G, Syrak SA, Stone DJ, Zierhut SD, Zhong H, Miller CB;  
PI Vernet KM, Wyse EA, Zerhusen BD, Zhong H, Miller CB;  
XX WTJ\_0003-116907/10.  
XX FDB\_0003-116907/10.  
XX NFD08 / ACT16880.  
XX  
XX New NOXV polypeptides and polynucleotides useful for treating or  
XX preventing e.g. cardiomyopathy, arrhythmias, hypertension, congenital  
XX heart disease, aortic stenosis, atrial septal defect, or atrioventricular  
XX canal defect.  
XX Claim 1: Page 173; 49pp; English.

CC ACNP6919 to ACNP7000 encode the human G protein-coupled receptor (GPCR)  
CC proteins, designated NOXV proteins, given in AR96130 to AB96491. The  
CC NOXV sequences can have cytotoxic, cardiovascular, antineoplastic,  
CC immunosuppressive, anti-HIV human immunodeficiency virus, hypertensive  
CC and/or other effects. The NOXV sequences are useful for treating or  
CC human diseases such as a pathology associated with the polypeptide, NOXV  
CC polypeptides, polynucleotides and antibodies can be used for treating or  
CC preventing e.g., aortic stenosis, atrial septal defect, atrioventricular  
CC canal defect, pulmonary stenosis, prostate cancer, uterine cancer,  
CC neoplasm, graft versus host disease, acquired immunodeficiency syndrome  
CC (AIDS), Crohn's disease, multiple sclerosis, or bronchitis. In some  
CC instances, the NOXV sequences may be used for identifying and isolating  
CC individual from minute biological samples (tissue lysate), and in  
CC representative identification of a biological sample. ACNP1001 to ACNP7117  
CC represent PCR primers and probes for the NOXV sequences, which are used  
CC in an example from the present invention.

XX Sequence 984 Aa:  
SQ

[illegible][illegible]

DB 480 SREGLSL--GRACNDWPPFGAGCHFPDAGCLYSNQCHVAPKAVIC---574  
 QY 349 RHLNDQALCHETDQLGSGRLVFLVLDGTGVKMSGRCSVLVETPIAVNG 408  
 DB 535 ---SNQAGLHTDPLQSG--LFLVLDGTGVKMSGRCSVLVETPIAVNG 590  
 QY 409 RNSNGPSPFSSCGGVYTFRRQCNPPAFQBGACVQADQAKNCTQACEKQLSF 468  
 DB 591 RNSNGPSPFSSCGGVYTFRRQCNPPAFQBGACVQADQAKNCTQACEKQLSF 620  
 QY 469 YRQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQV 511  
 DB 621 -----YRQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQV 669  
 QY 512 AIGSPIMKGLDPLDTKMSGPRDGTSLVSGSTFTFCQDMSQDQVQDQVQDQV 571  
 DB 670 AIGSPIMKGLDPLDTKMSGPRDGTSLVSGSTFTFCQDMSQDQVQDQVQDQV 729  
 QY 572 GDNSTSC-----SPKSGFTA-----GRABSTFTLT 588  
 DB 729 GDNSTSC-----SPKSGFTA-----GRABSTFTLT 789  
 QY 599 VFMVTSYIANRPLFLAVRIGRYVWAGMSISNTYVTSLLSDRVRVYALRSD 658  
 DB 790 TSP-----TPAFICQLPQASVQDQVQDQVQDQVQDQVQDQVQDQV 833  
 QY 699 RLPLRLHIMGLEDASL--QYRRYGVGGT-RP--ITFYQVQVQVQVQV 712  
 DB 834 SLFSTTQ--GSPVQMSALSSLSHGQVQVQVQVQVQVQVQVQVQVQVQV 890  
 QY 713 AVQPSVQV 772  
 DB 891 AVQPSVQV 906  
 QY 773 DQPCASQV 825  
 DB 907 -----GLHSTACVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 948  
 RESULT 14  
 ID AAU97642 standard; protein; 364 AA.  
 AC AAU97642  
 AC AAU97642;  
 DT XX 27-OCT-2002 (first entry)  
 DT XX Human Ha011374 protein.  
 XX Aggrenase; osteopathic; antiarthritic; antiinflammatory human;  
 KW cartilage; osteoarthritis; inflammatory disease; enzyme; Ha011374.  
 OS Homo sapiens.  
 XX XX XX020033093-92.  
 XX XX 25-APR-2002.  
 PD 17-OCT-2001; 2001NC-U0902458.  
 PR 18-OCT-2000; 2000US-0241469P.  
 XX (GENB ) GENETICS INST INC.  
 XX XX  
 PI Racie LA, Twine NC, Apostino MU, Wolfman NM, Morris EA;  
 NP1; 2002-454602/48.  
 DR N-PDB; AB052580.  
 XX XX  
 XX Novel purified aggrecanase polypeptide useful for developing inhibitors  
 TT and antibodies to aggrecanase polypeptide, which are useful for  
 PT treating aggrecanase-associated condition such as osteoarthritis.  
 XX

PS Discloure; Page 37-38, 41pp; English.  
 XX This invention relates to the cDNA and protein sequences of a novel human  
 CC aggrecanase polypeptide, and methods for preparing recombinant proteins to  
 CC apply the proteolytic activity of aggrecanase, or to inhibit the  
 CC aggrecanase-mediated cleavage of aggrecan in cartilage. The protein of  
 CC the invention is useful for developing inhibitors of aggrecanase protein.  
 CC The invention also provides a method for identifying aggrecanase genes  
 CC useful for designing probes for obtaining polypeptide sequences encoding other  
 CC aggrecanase molecules. The cDNA sequence is also useful for detecting  
 CC mRNA encoding aggrecanase in a given cell population, and thus for  
 CC identifying aggrecanase-expressing cells, tissues, organs, or  
 CC disorders involving cellular, organ or tissue disorders in which  
 CC aggrecanase is irregularly transcribed or expressed. The DNA sequences  
 CC may also be useful for preparing vectors for gene conditional applications.  
 CC The invention also provides a method for identifying aggrecanase genes  
 CC characterized by degradation of articular cartilage, by blocking the  
 CC enzyme's proteolytic activity. An aggrecanase protein inhibitor and a  
 CC method for inhibition of its activity are also described. The present  
 CC method for inhibition of its activity is useful for treating and other  
 CC inflammatory diseases. The present sequence represents the human  
 CC Ha011374 protein of the invention  
 QY Sequence 364 AA.  
 Query Match 23.2%; Score 1799; DS 5; Length 364;  
 Best Local Similarity: 100%; Positives 100%; Identical 100%;  
 Matches 329; Conservative 1; Mismatches 0;  
 QY 352 LDMGALSCHTDPLDQSGRLVFLVLDGTGVKMSGRCSVLVETPIAVNGMS 411  
 DB 1 NMOGALSCHTDPLDQSGRLVFLVLDGTGVKMSGRCSVLVETPIAVNGMS 60  
 QY 412 SNQPSFSSCGGVYTFRRQCNPPAFQBGACVQADQAKNCTQACEKQLSF 471  
 DB 61 SNQPSFSSCGGVYTFRRQCNPPAFQBGACVQADQAKNCTQACEKQLSF 120  
 QY 472 QCATQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQV 531  
 DB 121 QCATQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQVQDQV 180  
 QY 532 MNSGPRDGTSLVSGSTFTFCQDMSQDQVQDQVQDQVQDQVQDQVQDQV 591  
 DB 181 MNSGPRDGTSLVSGSTFTFCQDMSQDQVQDQVQDQVQDQVQDQVQDQV 240  
 QY 592 EYVTFYVTSYIANRPLFLAVRIGRYVWAGMSISNTYVTSLLSDRVRVY 651  
 DB 241 EYVTFYVTSYIANRPLFLAVRIGRYVWAGMSISNTYVTSLLSDRVRVY 300  
 QY 652 RVALTERRPLRHSITVHGFQADQVQ 680  
 DB 301 RVALTERRPLRHSITVHGFQADQVQ 329  
 RESULT 15  
 ID ABP43989 standard; protein; 364 AA.  
 AC ABP43989  
 AC ABP43989;  
 DT XX 26-FEB-2003 (first entry)  
 DT XX Procollagen I N-proteinase.  
 XX XX  
 KW Neuroprotective; immunomodulator; cancer; chromosome 3p14; cytotoxic;  
 KW ulcer; Alzheimer's disease; Huntington's disease;  
 KW ankyrotrophic lateral sclerosis; autoimmune disorder; inflammation;  
 KW vulnary.  
 XX XX  
 OS Bos taurus.  
 XX XX0200231111-42.  
 PW



Search completed: March 13, 2004, 07:39:00  
Job time : 216.239 secs





541. VMDQVCGGNCSTCFKAGSTAGABEVTVTLVTHLTSVITANRBLPFLHALVIG 600  
 624 GRVYAGGNSINTVTSGLDEORVETVALDEORLEIRIRINCPGDAIQTR 683  
 601 GRVYAGGNSINTVTSGLDEORVETVALDEORLEIRIRINCPGDAIQTR 660  
 604 XYBQGLTRDITFTFQPKRQAVMAAATVPGSCAGLRWYVSCLOARKEIVE 743  
 661 XYBQGLTRDITFTFQPKRQAVMAAATVPGSCAGLRWYVSCLOARKEIVE 720  
 741 TQCCGQSQPAPHPACTLSPCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 803  
 722 TQCCGQSQPAPHPACTLSPCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 780  
 804 PRACRGAQQAVALLETQDFCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 863  
 781 PRACRGAQQAVALLETQDFCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 840  
 864 PVTGDSVBEKLPAPBPCVMSCPFGAGHLTASGEKAPFMWGSITGQAQNVTPA 923  
 841 PVTGDSVBEKLPAPBPCVMSCPFGAGHLTASGEKAPFMWGSITGQAQNVTPA 900  
 924 AGSSTVSCRGLEAPFLDQSLAVTVQEGGLQAGSSTVSCRGLEAPFLDQSLAVTV 983  
 901 AGSSTVSCRGLEAPFLDQSLAVTVQEGGLQAGSSTVSCRGLEAPFLDQSLAVTV 960  
 984 ACSTVSCRGVTVLTVQARAGHDEBETLLTQCCGLPBPVPCVAGQSLLTL 1043  
 961 ACSTVSCRGVTVLTVQARAGHDEBETLLTQCCGLPBPVPCVAGQSLLTL 1020  
 1044 LQPSASGLQTAGSACTVQDQDQVTFEAMALVPMASVCLLACTVAVTQV 1103  
 1021 LQPSASGLQTAGSACTVQDQDQVTFEAMALVPMASVCLLACTVAVTQV 1080  
 1104 WBCSTVSCGDIQGRHCTLQDQQAQVPAFDQCHQVPTVTCVAGQSLLTL 1163  
 1081 WBCSTVSCGDIQGRHCTLQDQQAQVPAFDQCHQVPTVTCVAGQSLLTL 1140  
 1164 HEEAAAPRTATPAG-----AGCGHSP 1189  
 1141 HEEAAAPRTATPAGLENGQALSPAPRLLQPSGVSQASACHLSP 1200  
 1190 GTTIDMGEGQAQCAVALGRPLEVTVLTVLSESLASACHLSP 1249  
 1201 GTTIDMGEGQAQCAVALGRPLEVTVLTVLSESLASACHLSP 1260  
 1250 TTSSTNTLVVQRCQRCQRTVLYVQGLQAPVPCVAGQSLLTL 1309  
 1261 TTSSTNTLVVQRCQRCQRTVLYVQGLQAPVPCVAGQSLLTL 1320  
 1310 NAGCCHFLVNAFAHAAHALANNGAGTSSVTLRPTGCHTAPRPOGVLYR 1369  
 1321 NAGCCHFLVNAFAHAAHALANNGAGTSSVTLRPTGCHTAPRPOGVLYR 1380  
 1370 SSSQGVNBSRGFTVXQAGLQGVTVLQSVTPVQSGVQSGVQSGVQSGVQSGV 1416  
 1381 SSSQGVNBSRGFTVXQAGLQGVTVLQSVTPVQSGVQSGVQSGVQSGVQSGV 1427

## RESULT 3

US-10-057-487-8  
 ; Sequence 8, Application US/10057487  
 ; Publication No. 2003/005313A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: Wyeth  
 ; TITLE OF INVENTION: Agglutination Molecules  
 ; CURRENT APPLICATION NUMBER: US/10/057,487  
 ; CURRENT FILING DATE: 2003-01-25  
 ; PRIOR APPLICATION NUMBER: 60/441,469  
 ; NUMBER OF SEQ ID NOS: 8-10-15  
 ; SOFTWARE: Patent in version 3.1

; SEQ ID NO 8  
 ; LENGTH: 1427  
 ; TYPE: PRF  
 ; ORGANISM: homo sapiens  
 US-10-057-487-8

Query Match  
 Similarity: 98.04; Score 7596; DB 14; Length 1427;  
 Matches 1392; Conservative 0; Mismatch 1; Indels 34; Gaps 83

Qy 24 MQUQPPACPCPLVCMVCTAGCPCLLQCGSPHFGQCLGAEPCANVSYSKQKPP 83  
 1 MQUQPPACPCPLVCMVCTAGCPCLLQCGSPHFGQCLGAEPCANVSYSKQKPP 60  
 Qy 84 PFGPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQ 143  
 81 PFGPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQ 120  
 Qy 144 GAGFVPLVWVLTTPPAPANTANKTSGLSVQSGCTINPEDTQSGMGLVYTR 203  
 121 GAGFVPLVWVLTTPPAPANTANKTSGLSVQSGCTINPEDTQSGMGLVYTR 180  
 Qy 204 FLELPQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQ 263  
 181 FLELPQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQPCQ 240  
 Qy 244 CGSPGSCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 303  
 221 CGSPGSCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 280  
 Qy 324 PGLVYENANQVQVAPGAPVACTARBLKQMAKSCHTDPOSSCSLLVPLQGTG 383  
 301 PGLVYENANQVQVAPGAPVACTARBLKQMAKSCHTDPOSSCSLLVPLQGTG 360  
 Qy 384 GYVNCCKGKGSVLEVPLAAVYKQWNSGSPSPSCGGGVYTERQCNTPRFGQ 443  
 361 GYVNCCKGKGSVLEVPLAAVYKQWNSGSPSPSCGGGVYTERQCNTPRFGQ 420  
 Qy 444 RACVQGLQALQVQ 503  
 421 RACVQGLQALQV 480  
 Qy 504 ALCHMPCVAGSFTVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 563  
 481 ALCHMPCVAGSFTVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 540  
 Qy 564 VQPCVQV 623  
 541 VQPCVQ 600  
 Qy 624 GRVYAGGNSINTVTSGLDEORVETVALDEORLEIRIRINCPGDAIQTR 683  
 601 GRVYAGGNSINTVTSGLDEORVETVALDEORLEIRIRINCPGDAIQTR 660  
 Qy 684 XYBQGLTRDITFTFQPKRQAVMAAATVPGSCAGLRWYVSCLOARKEIVE 743  
 661 XYBQGLTRDITFTFQPKRQAVMAAATVPGSCAGLRWYVSCLOARKEIVE 720  
 Qy 744 TQCCGQSQPAPHPACTLSPCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 803  
 721 TQCCGQSQPAPHPACTLSPCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 780  
 Qy 804 PRACRGAQQAVALLETQDFCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 863  
 781 PRACRGAQQAVALLETQDFCFPMVAUDVDFGCSAGCGLEBPVPCVAGQSLLTL 840  
 Qy 864 PVTGDSVBEKLPAPBPCVMSCPFGAGHLTASGEKAPFMWGSITGQAQNVTPA 923  
 841 PVTGDSVBEKLPAPBPCVMSCPFGAGHLTASGEKAPFMWGSITGQAQNVTPA 900  
 Qy 924 AGSSTVSCRGLEAPFLDQSLAVTVQEGGLQAGSSTVSCRGLEAPFLDQSLAVTV 983  
 901 AGSSTVSCRGLEAPFLDQSLAVTVQEGGLQAGSSTVSCRGLEAPFLDQSLAVTV 960

QY 984 ACSVSGRQVRLINVCARAKRDEGELLDTQCGQLRPERQACSLSPFRPKVNS 1643  
 DB 961 ACSVSGRQVRLINVCARAKRDEGELLDTQCGQLRPERQACSLSPFRPKVNS 1620  
 QY 1044 LQPSASAQGLTQARSVAVQDQGVQVWBAQAAVPEASVPLADCTYRWNVCT 1103  
 DB 1021 LQPSASAQGLTQARSVAVQDQGVQVWBAQAAVPEASVPLADCTYRWNVCT 1080  
 QY 1104 WECVSGCDGQIQRSDRTCLGQQAQVPAQFQRLPFWVWGCMAGFCVQGGTSLVP 1163  
 DB 1101 WECVSGCDGQIQRSDRTCLGQQAQVPAQFQRLPFWVWGCMAGFCVQGGTSLVP 1140  
 QY 1164 HEBAAPGHTATPAG-- 1189  
 DB 1141 HEBAAPGHTATPAGASLEWQAGQLLSPAPQPRLLLPQDSNVSQSAQSGLEUPT 1200  
 QY 1190 GTTMDGQQAQDCAVGRPLGEVTVLWVLESINSAGDMLWGLTWKRCQLEUPT 1249  
 DB 1201 GTTMDGQQAQDCAVGRPLGEVTVLWVLESINSAGDMLWGLTWKRCQLEUPT 1260  
 QY 1250 TSSKNTNLVVRQGRPGQVLLYRQSLAPPTFYRCDMLPGFWGIVGSPLESPAS 1309  
 DB 1261 TSSKNTNLVVRQGRPGQVLLYRQSLAPPTFYRCDMLPGFWGIVGSPLESPAS 1320  
 QY 1310 NAGCCLFLINVAHQALAHALATNNGAGTGKNAVSLTRTHSLTATPAGQVQVLE 1369  
 DB 1321 NAGCCLFLINVAHQALAHALATNNGAGTGKNAVSLTRTHSLTATPAGQVQVLE 1390  
 QY 1370 SSSQASRFESEFQAKQSLGGQVTLQSNVPEQDPSNGKRGST 1416  
 DB 1381 SSSQASRFESEFQAKQSLGGQVTLQSNVPEQDPSNGKRGST 1427

RESULT 4  
 US-0-222-334-4 Application US/1022334  
 Publication No. US20030073116A1  
 GENERAL INFORMATION: David  
 INVENTOR: Ginebro, David  
 APPLICANT: Galia  
 APPLICANT: Tsai, Han-Nou  
 TITLE OF INVENTION: ADAMTS-13 Genes and Proteins and Variants, and Uses Thereof  
 CURRENT APPLICATION NUMBER: US/10/222,334  
 PRIOR FILING DATE: 2002-08-16  
 PRIOR APPLICATION NUMBER: 60/112,834  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: Patent in version 3.1  
 SEQ ID NO 4  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-222-334-4

Query Match 46.6%; Score 3609.5; DB 14; Length 842;  
 Best Local Similarity 77.1%; Pred. No. 2.5e-257;  
 Matches 712; Conservative 20; Mismatches 90; Indels 101; Gaps 16;  
 QY 214 WHQRPFRACPVAVGILACQIFLQCGHSPQSCQALPQANSTSLSPQALKRP 83  
 DB 1 WHQRPFRACPVAVGILACQIFLQCGHSPQSCQALPQANSTSLSPQALKRP 60  
 QY 84 PSFQQRQRQRARAGGLLELLVAVGVDFVQFQHETERYVNLNIGALELDEL 143  
 DB 61 PSFQQRQRQRARAGGLLELLVAVGVDFVQFQHETERYVNLNIGALELDEL 120  
 QY 144 GACPVHVLNVLITPEGANTANLSTSLSCVGSQSTNPEDTQPOHALLVYTR 203  
 DB 121 GACPVHVLNVLITPEGANTANLSTSLSCVGSQSTNPEDTQPOHALLVYTR 180  
 QY 204 FQLELFDQNSQVQVQLQGLGASPTFNSCLTETDQFQZLVTAHETGHSFGLHDAQFS 263

RESULT 5  
 US-09-781-0809-11  
 Sequence 11 Application US/097810809  
 Patent No. US2002014349A1  
 GENERAL INFORMATION:  
 INVENTOR: HOLLOWAY, JIM  
 APPLICANT: HOLLOWAY, JIM  
 APPLICANT: YAMAMOTO, GAYLE  
 TITLE OF INVENTION: Anti-Agiogenic Intestinal Peptides,  
 TITLE OF INVENTION: adint5  
 CURRENT APPLICATION NUMBER: US/09/781,080B  
 CURRENT FILING DATE: 2002-01-30  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patent Pending for Windows Version 3.0  
 SEQ ID NO 11  
 LENGTH: 1120  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: VARIANT

DB 181 FQLELFDQNSQVQVQLQGLGASPTFNSCLTETDQFQZLVTAHETGHSFGLHDAQFS 240  
 QY 264 GQSPGHVNAQAGLADGLADLSPQSLQELLAGACAACTWDPFPGSPGSAHQPDQA 323  
 DB 241 GQSPGHVNAQAGLADGLADLSPQSLQELLAGACAACTWDPFPGSPGSAHQPDQA 300  
 QY 334 POLYTSANEQVAVPFAVAVCFABEHLMDQALCHSTDFLQSCSLRLFLPLDQTEC 383  
 DB 301 POLYTSANEQVAVPFAVAVCFABEHLMDQALCHSTDFLQSCSLRLFLPLDQTEC 360  
 QY 384 GTVMCKRQKDSLVETFTIAVHVSWSKGFPRQSCAGGVQVTRSCNNRPAQG 443  
 DB 361 GTVMCKRQKDSLVETFTIAVHVSWSKGFPRQSCAGGVQVTRSCNNRPAQG 420  
 QY 444 RACVADALAKMNTQVQVQVLEMSQCCQVLPASQSPGASFGFHWGAVPHSQD 503  
 DB 421 RACVADALAKMNTQVQVQVLEMSQCCQVLPASQSPGASFGFHWGAVPHSQD 480  
 QY 504 ALGKMKALGDSFTWEGDSFTLQMSGSEDFEETLSCTGSCCTTCGCGMSQ 563  
 DB 481 ALGKMKALGDSFTWEGDSFTLQMSGSEDFEETLSCTGSCCTTCGCGMSQ 540  
 QY 564 YQSGVQGDQNSGKSPGSLQCTGCHSPGSEDFEETLSCTGSCCTTCGCGMSQ 623  
 DB 540 YQSGVQGDQNSGKSPGSLQCTGCHSPGSEDFEETLSCTGSCCTTCGCGMSQ 504  
 QY 600 VADQVQGDQNSGKSPGSLQCTGCHSPGSEDFEETLSCTGSCCTTCGCGMSQ 654  
 DB 571 VADQVQGDQNSGKSPGSLQCTGCHSPGSEDFEETLSCTGSCCTTCGCGMSQ 540  
 QY 624 GRVYQKQNSKSNPTVYSLLEQCHRYEVALTDETLPRLETRIMQPLQEDATQVY-- 681  
 DB 601 GRVYQKQNSKSNPTVYSLLEQCHRYEVALTDETLPRLETRIMQPLQEDATQVY-- 660  
 QY 682 RFEQSGVQL-----TEPDITFTYFKPRQVNAVAVTPGSCVAGLKNVNSCLD 735  
 DB 661 RFEQSGVQL-----TEPDITFTYFKPRQVNAVAVTPGSCVAGLKNVNSCLD 700  
 QY 736 QAKELVETVQCGSQDQPPAMPACTLECPYPVAVGDFQSCAGCLBRPVEVCEA 795  
 DB 713 QAKELVETVQCGSQDQPPAMPACTLECPYPVAVGDFQSCAGCLBRPVEVCEA 746  
 QY 796 QGSLKTLFPACAGAQPAVALETQNPQAPVSESPSCTSAQAGLALENETCV 855  
 DB 771 QGSLKTLFPACAGAQPAVALETQNPQAPVSESPSCTSAQAGLALENETCV 820  
 QY 856 PQADGLAEVTPGSGVTEKL-PAPERCVGMPQGMQLNLSAGEKASPMQSTQCA 914  
 DB 827 PQADGLAEVTPGSGVTEKL-PAPERCVGMPQGMQLNLSAGEKASPMQSTQCA 880  
 QY 915 QKAVY-WT-NAGKSSVSCGG 934  
 DB 813 QKAVY-WT-NAGKSSVSCGG 834



TYPE: amino acid  
 STRANDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-09-978-979-5

Query Match: 33.2%; Score 1799; DB 9; Length 365;  
 Local Similarity 99.7%; Pred. No. 2.8e-124;  
 Matches 338; Conservative 1; Mismatches 0; Gaps 0;

351 LKMOALSCHTPDQSSGSLVPLDGTGCVKMKSGKSLVLTPIAVHGRMS 411  
 412 SNQPSFSCSGCGVVTTRQCNFRPAFGACVAGLQAKMONTCAKCTQLEPMSQ 531  
 532 MSRGDEGDTLSLCHSGSRTFGCGMGMGQVWRCVCGDNSTCPKSPFTAGBAR 591  
 592 EYVTEVTPNLTSLVANSRPFTHLAVRIGRYVAGMGSISNTTVPSELDERVEY 651  
 651 MSQPRGDTLSLCHSGSRTFGCGMGMGQVWRCVCGDNSTCPKSPFTAGBAR 240  
 241 EYVTEVTPNLTSLVANSRPFTHLAVRIGRYVAGMGSISNTTVPSELDERVEY 300  
 301 RVALTEEDLPLESLRWPLQEDADGV 680  
 680 RVALTEEDLPLESLRWPLQEDADGV 329

RESULT 8  
 US-09-978-979-6  
 Sequence 6, Application US/0978979  
 TITLE OF INVENTOR: American Home Products Corporation  
 NAME OF INVENTORS: Morris, Elisabeth  
 ADDRESS: American Home Products Corporation  
 STREET: One Campus Drive  
 CITY: Fairfield, New Jersey  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07004  
 COMPLETION DATE: 1997-05-05  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 SOFTWARE: GENSCAN, GENSCAN 1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/979,979  
 FILING DATE: 2002-01-25  
 PRIORITY DATE: 2002-01-25  
 CLASSIFICATION: C07K 16/00  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/60/241,469  
 FILING DATE: 1997-05-05  
 ATTORNEY AGENCY INFORMATION:  
 NAME: Kaplin, Ellen J.  
 REGISTRATION NUMBER: 32,345  
 TELECOMMUNICATION INFORMATION: GI 54359  
 TELEPHONE: (973) 660-5000  
 TELEFAX: (973) 683-4117  
 INFORMATION: (973) 683-4117  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 738 amino acids  
 TYPE: amino acid  
 STRANDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-978-979-6

Query Match: 18.8%; Score 1459.5; DB 9; Length 738;  
 Local Similarity 39.4%; Pred. No. 7.9e-99;  
 Matches 374; Conservative 34; Mismatches 430; Gaps 32;

252 SGLGKAPKSGCGVVTTRQCNFRPAFGACVAGLQAKMONTCAKCTQLEPMSQ 288

TYPE: amino acid  
 STRANDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-09-978-979-5

Query Match: 33.2%; Score 1799; DB 9; Length 365;  
 Local Similarity 99.7%; Pred. No. 2.8e-124;  
 Matches 338; Conservative 1; Mismatches 0; Gaps 0;

351 LKMOALSCHTPDQSSGSLVPLDGTGCVKMKSGKSLVLTPIAVHGRMS 411  
 412 SNQPSFSCSGCGVVTTRQCNFRPAFGACVAGLQAKMONTCAKCTQLEPMSQ 531  
 532 MSRGDEGDTLSLCHSGSRTFGCGMGMGQVWRCVCGDNSTCPKSPFTAGBAR 591  
 592 EYVTEVTPNLTSLVANSRPFTHLAVRIGRYVAGMGSISNTTVPSELDERVEY 651  
 651 MSQPRGDTLSLCHSGSRTFGCGMGMGQVWRCVCGDNSTCPKSPFTAGBAR 240  
 241 EYVTEVTPNLTSLVANSRPFTHLAVRIGRYVAGMGSISNTTVPSELDERVEY 300  
 301 RVALTEEDLPLESLRWPLQEDADGV 680  
 680 RVALTEEDLPLESLRWPLQEDADGV 329

RESULT 7  
 US-10-057-487-5  
 Sequence 5, Application US/1007487  
 TITLE OF INVENTOR: American Home Products Corporation  
 NAME OF INVENTORS: Morris, Elisabeth  
 ADDRESS: American Home Products Corporation  
 STREET: One Campus Drive  
 CITY: Fairfield, New Jersey  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07004  
 COMPLETION DATE: 1997-05-05  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 SOFTWARE: GENSCAN, GENSCAN 1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/057,487  
 FILING DATE: 2002-01-25  
 PRIORITY DATE: 2002-01-25  
 CLASSIFICATION: C07K 16/00  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/60/241,469  
 FILING DATE: 1997-05-05  
 ATTORNEY AGENCY INFORMATION:  
 NAME: Kaplin, Ellen J.  
 REGISTRATION NUMBER: 32,345  
 TELECOMMUNICATION INFORMATION: GI 54359  
 TELEPHONE: (973) 660-5000  
 TELEFAX: (973) 683-4117  
 INFORMATION: (973) 683-4117  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 738 amino acids  
 TYPE: amino acid  
 STRANDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
 US-10-057-487-5

Query Match: 33.2%; Score 1799; DB 14; Length 365;  
 Local Similarity 99.7%; Pred. No. 2.8e-124;  
 Matches 328; Conservative 0; Mismatches 0; Gaps 0;

352 LKMOALSCHTPDQSSGSLVPLDGTGCVKMKSGKSLVLTPIAVHGRMS 411  
 412 SNQPSFSCSGCGVVTTRQCNFRPAFGACVAGLQAKMONTCAKCTQLEPMSQ 471





Qy 473 CARDQGF-LASSPGASFTENGAAYPHQDNDLCHRMCAIGBIFMRGDSFLQTRIC 531  
Dy 238 VNRSGARVRNAPQ-----INSXPAPQ-----C 261  
Qy 532 MFSPEFEDTGLSVCBGETTCGQDMOSQVQWQVQCOGQUNSTCSFSGSTFAGAR 591  
Dy 262 MABQ-----LQVTEVQ-----APAPAEV-----SFGESAT-----290  
Qy 592 EVTFVITVTLVSTVIANRHLRPLFLVLRVGVVAGMISSEVITVTSLLDQVRY 651  
Dy 291-----TQDQ-----LQVTEVQ-----290  
Qy 652 RVATEDLRLPRLREIR--IMPLQEDAQVRYRGVEYONVTRPDITTFQFQKRW 709  
Dy 303 -VLISPRCATAPAPRPSNCSNSGEPFASRAPP--LAAP-----BSTTQVL 350  
Qy 710 VNAVAPG-GEVCGAGLRWYVSCLDQARKEIVTQVQSGQPPAPPEACVLEPCPT 768  
Dy 351 LVTNAGKACADQOPLA-----RASBXVTSATSG-----DQVQVAP-----391  
Qy 769 MAVDQGP-----CSASG-----GQLRR-----PVCV-----BAGLLK-----801  
Dy 392 ---GDTQFACVCEALNGLNVMWVPSVQVQVQVQVQVQVQVQVQVQVQVQVQV 448  
Qy 802 ---TUPA-----PCRAQA-----OFA-----VALETCN 823  
Dy 449 SRFQPLPTXVSTLPTGLSBHTWQSGEAMSGEXASLPPTPSPWVWVSTW 508  
Qy 824 PGP-----CPA-----RMVSESSCTSAGACALENETCFQADGLAP 864  
Dy 509 PSPTATCAVRSNGSPSKML-SRWVSEPSCTSAGACALENETCFQADGLAP 568  
Qy 865 VTGFSQDEKLPAPEFCVQWCPQGHLDATSGEADSGSWSITTAJAAVWTPA 924  
Dy 569 VTGFSQDEKLPAPEFCVQWCPQGHLDATSGEADSGSWSITTAJAAVWTPA 628  
Qy 925 GEVCEVQGLMEFLFQSAJRVQBEELQALSPGSRVQVQVQVQVQVQVQVQVQV 984  
Dy 629 GEVCEVQGLMEFLFQSAJRVQBEELQALSPGSRVQVQVQVQVQVQVQVQVQ 688  
Qy 985 CVSCGQVVRVILYQVANGSDXBEELTQVQVQVQVQVQVQVQVQVQVQVQV 1034  
Dy 689 CVSCGQVVRVILYQVANGSDXBEELTQVQVQVQVQVQVQVQVQVQVQVQV 738

RESULT 10  
US-09-978-978-1

Sequence 1: Application US/09/97979  
Patent No. US2002011102A1  
GENERAL INFORMATION:  
APPLICANT: Racie, Lisa, A.  
Apollonio, Michael, J.  
Twine, Natalie, C.  
Morris, Elizabeth

TITLE OF INVENTION: Aggrucanase Molecules  
NUMBER OF SEQUENCES: 6  
COMMENTS: Aggrucanase

ADDRESS: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: NJ  
COUNTRY: USA

ZIP: 07054  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
CURRENT APPLICATION DATA: Release 11.0, Version #1.30  
APPLICATION NUMBER: US/09/978,979  
FILING DATE: 16-Oct-2001

CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
FILING DATE: US/60/241,469  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaplow, William J.  
FIRM: Kaplow, William J.  
REFERENCE/DOCKET NUMBER: GI 5435P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (973) 860-5000  
FAX: (973) 860-5017  
INFORMATION FOR SEQ ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
STRANDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
FUNCTION: unknown  
MOLECULE DESCRIPTION: SEQ ID NO. 1:  
US-09-978-979-1

Query Match 16.3% Score 1261; DB 9; Length 242;  
Best Local Similarity 100.0%; Pred. No. 7,6e-85;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SCQALPEQAVSEVYSPGAKRPPSPFQQRQRRAGILHLLVAVGQVQPA 118  
Dy 3 SCQALPEQAVSEVYSPGAKRPPSPFQQRQRRAGILHLLVAVGQVQPA 62  
Qy 119 HDEETVYVLTNAINGLRPSGAGQVRLVWVLTTPESGAPNTANTTSLSVC 178  
Dy 63 HDEETVYVLTNAINGLRPSGAGQVRLVWVLTTPESGAPNTANTTSLSVC 122  
Qy 179 QMGVQV 238  
Dy 123 GAGCTTNPEDTFCRAVLVLTTPLEPQNRVQVQVQVQVQVQVQVQVQ 182  
Qy 239 FEGCTTANEGHAFSGVQSGGQSGGQSGGQSGGQSGGQSGGQSGGQSG 297  
Dy 183 FLQVLTANEGHAFSGVQSGGQSGGQSGGQSGGQSGGQSGGQSGGQSG 241

RESULT 11  
US-10-057-487-1

Sequence 1: Application US/2005/487  
Patent No. US2006005053A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth

TITLE OF INVENTION: Aggrucanase Molecules  
NUMBER OF SEQUENCES: 2  
COMMENTS: Aggrucanase

ADDRESS: Wyeth  
STREET: 500 Locust Street  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA

ZIP: 19106  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows NT/2000  
CURRENT APPLICATION DATA: Release 11.0, Version #1.30  
APPLICATION NUMBER: US/05/487,979  
FILING DATE: 16-Oct-2001

Query Match 16.3% Score 1261; DB 14; Length 242;  
Best Local Similarity 100.0%; Pred. No. 7,6e-85;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 SCQALPEQAVSEVYSPGAKRPPSPFQQRQRRAGILHLLVAVGQVQPA 118  
Dy 3 SCQALPEQAVSEVYSPGAKRPPSPFQQRQRRAGILHLLVAVGQVQPA 62  
Qy 119 HDEETVYVLTNAINGLRPSGAGQVRLVWVLTTPESGAPNTANTTSLSVC 178  
Dy 63 HDEETVYVLTNAINGLRPSGAGQVRLVWVLTTPESGAPNTANTTSLSVC 122

179 QNGSTINPDDPQALVILVITDELFDONQVGTWGLAGSPFSLTETQ 238  
123 QNGSTINPDDPQALVILVITDELFDONQVGTWGLAGSPFSLTETQ 182  
239 FDLVATLHAGSLGSLRGLHAGSPGSGHWSAGAPLAGLMSGSRGLLSL 297  
183 PLDTVITLHAGSLGSLRGLHAGSPGSGHWSAGAPLAGLMSGSRGLLSL 241

RESULT 12  
US-10-240-545A-2  
Sequence 2, Application US/10240545A  
Publication No. US20030185928A1  
Applicant: Yamanouchi Pharmaceutical Co., Ltd.  
Title of Invention: No. US20030185928A1, aggrcanease  
File Reference: 08495.0002 US/0740.545A  
Current Filing Date: 2002-10-02  
Prior Filing Date: PCT/JPO/11/033  
Prior Filing Date: 2001-12-17  
Prior Filing Date: 2000-06-03  
Prior Filing Date: 2000-12-18  
Number of SEQ ID NOS: 26  
SEQ ID NO 2: 221  
Type: PCT  
Organism: Homo sapiens  
US-10-240-545A-2

Query Match  
Best Local Similarity 28.4%; Pred. No. 1, 1e-78;  
Matches 312; Conservative 139; Mismatches 409; Indels 27; Gaps 36;

94 RORAAQGI--LHLELLVAGPDPQAH-QETERYVLNUNIGALLPGLQAPV 149  
281 RPRSAQSGKQGVETVLVAKQKVGKGVNVTILVWNVGSLPQDGTGSDIN 340  
150 HLVRVVLTEPGANITAAVIGSSVGSQSTINPDDPQALVILVITDEL 208  
341 VVSELILBSPGLLHNAQGLSLFQWGSALGALOKKQKHNA---ILTFQDLSN 397  
209 PGNRQVGVGTQAGACFMSCLITDTPGLVGTIARIHSLPGLHAGSGQGR 268  
398 KNEPCTDPAFISQNGKRYCTETHTGLGLATHAGSNGFMHDI-ENPCKRA 456  
269 -GHVNASGAPAGLANSPCRRQLLSLACRANCWPPRPGSAGHPAQAQPL 327  
457 ENHPTLGNAGVYMSKCTQKLTFTQAGCLVDFK-QAQTKY-PDLQPL 514  
328 YANQGVAPQVAPKAT--FAHSLHLCALSCHTDPLASLLVLLVLEDTQ 385  
515 YADCTQAPQAKAKSLQFVK--DICKSARH--VQRIETKPAAPQVTCUL 568  
386 EWSKGRKSELVETAAVIGHMSNPGRSPCSGGVGTTERQCNTPRAFGZA 445  
569 SMWQCGQVXQFQGL-RTFQHGVMKMSNSKCATCGVYKRVHNCNPFQFQ 627  
446 CVGADQAKENQWQAKCTQWGSQACATDQGLASGSGFVHCAVHISGQAL 505  
628 CFSGSIYVLNINFCNPSLQPAQVATNPKF-----GMYQMTPTVYEEER- 681  
506 CEMWALGSEFMISGSLFQTRCNPSRDEDTSLVCSGCTCCGCGMOSQW 565  
682 CLYICAKANPEFPMKGVKQVGPCKSR--IND-----VCLDQVCGHSLGASZ 735  
566 DRCVQGGDNSTCSRPSGF-TAGRAEYVIVITFVNLVSIANRPLPVLAV 10 623  
736 DAGCVQMDNCTCFYGLVGNKATNHYFVVIIPAGARSLCELOVSSSLVAG 795  
624 GRVYVAGNISPNTVSELGSEVVERVALTERPLERLEHINWPLQEDQIVR 683

796 QXYLTGMSLWQDPSF--FAGITTFVQSEN-----RPRLYAGPTNTEVFLQ 848  
684 YQREUHLREDDTPTDYOK-----PQKATNATGCGTSCGACLRNYSGL 734  
849 -GK-----NGIAYKALFKVAGTTPATPAPVMSVIGSCVSGCGVNVWALCL 901  
735 DQAKVETVQCGSQGQDPAKCYLCEPFPFVAGPQSPQSGAPKRPYQV 794  
902 RQNTQV-VNSESCTANPTTPTCTCAGTCFVWNPENGTCSAGAGQCSHAKTCVQ 960  
795 AGSELITTPRACRQAGQAPVALFECVPCQFPAHNVGSPSSCSAGAGLALNENCT 854  
961 -----KFPKREAVHSLCP-----VSTPTQV----- 983  
855 VPGAGLEAPVTEGSPVDEKLPABKCVQKSGQCPQCHLALASGEKASPKWSIKTGA 914  
984 -----QACNHSKCPQW-----SIG-----PW----- 1000  
915 QANVTTPAARCSVSCRGELMELRFTQNSGALRYVUELCLASVGSRETCVAPCF 974  
1001 -----SCKSCRGVREGLCKGSA----- 1022  
975 PAHQVVLKASVCGCGVRYLILYUAGHEDDQREILDTQCOGLPRRBPQASLSP 1034  
1023 -----AETLPSSQCTSLRPLQGVQCR 1047  
1035 GCP-----RNVKNSLQPSASGCLZPARSVACVQLCQGVVREACALVPRASVP 1089  
1048 CQNSRLQWASSHSCATCGVLRKEMKSEKFGKLTFFPCRCNTKZKMLD-- 1105  
1090 CLTACTYR-----HNGVNMCSVCGCGLQRESDTCLPQCAQVPAQCF 1136  
1106 -LEETCRQACFAPVTVWVAGVSLPMLQCTVTCGQVTRSEVVCV-----QQRSESSC 1160  
1137 QMLPVTYTGQMAQCF 1153  
1161 LHQKFPVLRACNTNFC 1177

RESULT 13  
US-08-972-467-2  
Sequence 2, Application US/0997467  
Publication No. US20030185928A1  
General Information:  
Applicant: PFIZER INC.  
Title of Invention: ADAMS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
FILE REFERENCE: PCL0852A  
CURRENT APPLICATION NUMBER: US/09/972,467  
CURRENT FILING DATE: 2001-10-05  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2:  
Length: 1629  
Organism: Human  
US-08-972-467-2

Query Match  
Best Local Similarity 25.5%; Pred. No. 1, 7e-77;  
Matches 348; Conservative 170; Mismatches 505; Indels 343; Gaps 50;

89 QPQGRQGRBAGGTLHLLVANGDPVFAHQBQRTVRLNUNIGALLPGLQAPV 148  
279 KETRTKTFJSTPFTVTVVADNRVSVYHQLQVILTMSVAGISVQDINLIN 338  
149 VHLVQVVLTEPGANITAAVIGSSVGSQSTINPDDPQALVILVITDEL 206  
339 IIVNLVILHNBQCGHSCSPNAGTTLTANCOMHNSH-----SPQGHDTAVLPHDI 393  
207 EPLQNGVQVTCQGLAGSPGSGHWSAGAPLAGLMSGSRGLLSL 297  
394 CLHAKDCTQLAGLQCTCDPVYRSCISBDSGLSTAPTAHMLGAVNPNPD--DNKKCK 451



QY 207 ELPOGROVGVYQMGACPTNSCLITEDPGDVLGVITIAHIGHSFLEHDAQPSGCG 266  
 DB 375 CRANDKOTGLAELGTLCPYASCSISDSELSSTAFTHLEHGVNPNPD -DNICK 432  
 QY 267 PEG-----HYMADGAAAPAGLANSFCRQLGISAGACACWDPFPGAGHP- 320  
 DB 433 EGVGVSGQVAVNPTVYPMWMSKSVKTYFLDVGQGLNLEHPSF-----YFL 488  
 QY 321 DAQGLVYANBQVAVNPKAVACTFAEHLMDQNSCHTDLQSGCRLVPLD 380  
 DB 488 VOLGELVNNVAKCGLLPQSGCVTFWQ-----CRKLVNNGVKGCTGCTFWAD 544  
 QY 381 TCEGVNCKRCSLVEUETPIAAHREWMSFMRSPFCRSGGVYTRKQNPRA 440  
 DB 545 TCEPQKCYGVTC--VPEKENVVPTDQSGMSFPCSTGCTGGLKTAJENPPEK 602  
 QY 441 FQGAQVGAQVGNMTCQKTLQPSHSGQVQVQVQVQVQVQVQVQVQVQV 500  
 DB 603 NGKTYCVBMSKFKSCTFLPKQKDFQCAQVQVQVQVQVQVQVQVQVQV 658  
 QY 503 QDGL-----CHUKVAGLGEFPHKQSGSGLQVQVQVQVQVQVQVQVQV 557  
 DB 659 SGLWMDKCLFQVWADTVQVLDVDTGTC-----GQDNQVQVQVQVQVQV 712  
 QY 558 RQGVQV 616  
 DB 713 VLNKSKRQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 769  
 QY 617-----HIAVR-----IQBNVYH-QMGSFPMPTTSLGDEKQVAVNLEP 662  
 DB 770 ETDQNTLQVLSKSGKEFLANQVQVQVQVQVQVQVQVQVQVQVQV 816  
 QY 663 HEIRHWQV 711  
 DB 817 VKNRSTORLQGLLOV-----SVGLNPNQVQVQVQVQVQVQVQVQV 870  
 QY 712-----QVGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 720  
 DB 871 LKSPCKRQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 930  
 QY 721 SCQGLKQV 775  
 QY 931 QCGVQV 988  
 QY 776 QSGASQV 935  
 DB 989 ECHNSQV 1041  
 QY 836 ECTBQV 990  
 DB 1042 MSLCVQV 1092  
 QY 892 QHLDASQV 951  
 DB 1093-----QAG-----QGVQVQVQVQVQVQVQVQVQVQVQVQV 1124  
 QY 952 EQLQGLASQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 993  
 DB 1125 DNDQV 1183  
 QY 994 VRLTYQV 1053  
 DB 1184 MSLCVQV 1237  
 QY 1054 QV 1098  
 DB 1238 GRATVQV 1294  
 QY 1099-----QVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1140  
 DB 1295 VTRFASQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1351  
 QY 1141 EPTVQV 1161

Query Match 14.98; Score 1157; DB 9; Length 1882;  
 Best Local Similarity 25.5%; Pred. No. 5,76-76;  
 Matches 346; Conservative 107; Mismatches 505; Indels 342; Gaps 52;

QY 89 QGQGVQV 148  
 DB 227 ECTREKTFSTFPTFVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 286  
 QY 149 VHLVQV 206  
 DB 287 ELPVQV 340  
 QY 207 QV 398  
 DB 341 CRANDKOTGLAELGTLCPYASCSISDSELSSTAFTHLEHGVNPNPD -DNICK 398  
 QY 267 PEG-----HYMADGAAAPAGLANSFCRQLGISAGACACWDPFPGAGHP- 320  
 DB 399 EGVGVSGQVAVNPTVYPMWMSKSVKTYFLDVGQGLNLEHPSF-----YFL 454  
 QY 321 DAQGLVYANBQVAVNPKAVACTFAEHLMDQNSCHTDLQSGCRLVPLD 380  
 DB 455 VOLGELVNNVAKCGLLPQSGCVTFWQ-----CRKLVNNGVKGCTGCTFWAD 510  
 QY 381 TCEGVNCKRCSLVEUETPIAAHREWMSFMRSPFCRSGGVYTRKQNPRA 440  
 DB 511 TCEPQKCYGVTC--VPEKENVVPTDQSGMSFPCSTGCTGGLKTAJENPPEK 568  
 QY 441 FQGAQVGAQVGNMTCQKTLQPSHSGQVQVQVQVQVQVQVQVQVQVQV 500  
 DB 569 NGKTYCVBMSKFKSCTFLPKQKDFQCAQVQVQVQVQVQVQVQVQVQV 624

RESULT 15  
 US-09-816-171A-13  
 ; Sequence 13; Application US/09816.171A  
 ; Patent No. US/20010108941  
 ; INVENTOR: J. C. Snel  
 ; APPLICANT: Aps  
 ; APPLICANT: Hurskainen, Tiina L.  
 ; APPLICANT: Michrath, Satohi  
 ; FILE REFERENCE: 264/304195 Acids Encoding Zinc metalloproteases  
 ; CURRENT APPLICATION NUMBER: US/09/816.171A  
 ; CURRENT FILING DATE: 2001-07-30  
 ; PRIOR FILING DATE: 1999-08-06  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ. LENGTH: 1882  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens ADAMTS-9  
 ; NAME/KEY: MOD RES  
 ; LOCATION: (468)  
 ; OTHER INFORMATION: Xaa = Cys  
 ; LOCATION: (122)  
 ; OTHER INFORMATION: Xaa = Tyr  
 ; US-09-816-171A-13

501 QODAL---CRHVKALGBSEFMKRGDSFLDGTQKNSGPREDTGLSLCTYSKSCRTGCGD 557  
 625 SGLIMURCZCFRVAHNTATYKQURVTDGTPC-----CQDNDICVQLCQKQCMH 678  
 558 RMDSQMDQVQOQDQNSCTPKRGKSTAGRAKSEYVTFVFNLSYVIANHRLPT- 616  
 679 VLNKARUKQVQOQDQNSCTVAGTFNTH-YGVNVTYFAGNLDVQKGS-FSG 735  
 617 -----HLAVR-----IGERYVA-GMGISPNITTFSLBGRVYRVALTEDRLPR 662  
 736 ETDQNTJALSSKGEFLNAGVFNAGLIR-----JGNVYLSGSET-----A 782  
 663 LBEBIRWGLQDQNTQVTRTGEYGNTRPDIFTY---EOKFPRQM-----WAVY 714  
 783 VERINSTRJGBLJQVIL-----SVGLVNEVYRISFNPIEDKQVQVNSHGWKAC 837  
 715 RQFC-----SVS-----CGAG-LRW-----728  
 838 SKYQOBERKVCYTRBESQVLYDQRCBLPQCHLITFCVQCDLKNVYASRSCAQ 897  
 729 -----VNTSLDQAKELVETVQOQSQOPNMPBACVLEPCFPVAVDQFP 776  
 898 OGLSVYTDILCAKATSLD-GKENTDQSPC-SNPKFSNKGSCENTGQWYKANTE 955  
 777 QASQGLURERFVYQVQASLKLTPAPRCQAGQAPVAVLETQFPQCPANVEVREP 836  
 956 CKSJCTQGTQGBAFCVNTXNOV---LJDSKC---THKXVYTCRSEFPCT-QNSQDOW 1008  
 837 SECTSAGACALANETCVFQADQLAPVTPGQGVNKEJAPCPQVMSCP---PQWQ 892  
 1008 SBLVTCGKHHSQVWQVQERJADQWCD-----PEYPTSNVQVQPCASW- 1058  
 893 HLDATGEMAPSPGSIETGAQANTWTPAAGSVSGQJMEIRFLZQMSALRPVQ 952  
 1059 -----QAG-----PK-----VQESTQDQVQLAVKCIOTWASVD 1091  
 953 BELGLAKSGSRREVQVQVPC--PA-----EMQV-KLAAGSVSGQVY 994  
 1092 DNDQNAHRTPTQD-LELPSCHFPALPBTASTYAPSTQMGKFSWPCSTKSKZTA 1150  
 995 RRLVLCBAGAGDDBELITQOGLRPPQPCALEPCPPKMNLSLQPCNSCGL 1054  
 1151 HWYNSC-----RBNQSVQBSANLIRVAKESCVTC-QQWALDMSLSCVTCQD 1204  
 1055 HWNSVACVQDQGVQDEBACALVPRASVFLTAICTYR-----1098  
 1205 BAKTRQWVNY---SHVYJRESEQDQVTPETQDQNSPCFQRTSGSLAQHFPQEDY 1261  
 1099 -----HWNTWMECSVCDDIQRRTDGLQQAQVVPQFQHLPX 1141  
 1262 RPRASPSFHVGLGNQWTFMGACSTAGSQRHVVC---QDQNYTANDYERIK 1318  
 1142 PTVYRQWAGPCV-----QDQTSIL-----1161  
 1319 PBOBACSGSPQWAGWQCECTKGGHITRLVWSQNSRFPDLSCELLKEPDR 1378  
 1162 -----VHBEAARQPTTAPMAGCR-----QJLB-----PQOT 1191  
 1379 SQCHTACPDHAKNSTQVPMSSGCV-SCGRKHQRYTCWAGDSHLSYCYKHLAKPHH 1437  
 1192 IDMRQ-----PQADJVALGRPGVETLRYVLESLSKASG 1228  
 1438 KRCGRCPKXWAGANSQSVNKR-----GQGRNGTQIG 1474

Search completed: March 13, 2004, 08:07:02  
 Job time : 119.1 secs













Db 804 -ETVQZKPMFJNTGTYV-----FVQD-TXVLTUXTKXIHESLNDUNWVLEQSYV 856  
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 Db 857 EWALKNSCKKCGQSGQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 916  
 Qv 768 YNAGVPGCSAGCQ-GLGRPBYCYE-AGSLKLTFFAPKACQAQAPAVALETCFQ 825  
 Db 917 VNTGWMFQSGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 973  
 Qv 826 PCFARVNEVSESCSAGAGALANETVCVQALQLEAPVTEGSGVDSKLPAREFCV 885  
 Db 974 LCPJHMA----- 981  
 Qv 886 SCFEGHGLDZAGBZAPSPGSIPTGQAANVTPAAGSVSVSCRGJMEIFRIC-W 943  
 Db 982 -----GPN-----SCSCTCYTBEVFLDTA 1005  
 Qv 944 DSNALVFBVELGZKAFSGRSREVCVQPCAPQWYKLAASVSCRGVRRILCSA 1003  
 Db 1006 DQPT-QUE-----REFAT-TELQD-----RNI----- 1032  
 Qv 1004 HESDQDEILDTQCCQLPFPPEBGLKLEPCFPKWNKSLQPSACGLTPARSVAC 1062  
 Db 1033 -SPPKSEYV--VQWLSRPPDS-----PIKSEKHQD-----KSPC 1071

RESULT 7  
 / Sequence 11, Application US/09491522  
 / Patent No. 642898  
 / Applicant: Colgate, Charles M.  
 / Applicant: Lapierre, Charles M.  
 / Applicant: Prochop, Darwin J.  
 / Applicant: U.S. Patent & Trademark Office  
 / Title Of Invention: AND THE PRODUCTION, METHODS AND USES THEREOF  
 / Number Of Sequences: 17  
 / Correspondence Address: Edwards, LLP  
 / Street: 1155 Avenue of the Americas  
 / City: New York  
 / State: NY  
 / Zip: 10036-2811  
 / Computer Readable Form:  
 / Medium Type: Diskette  
 / Operating System: Windows  
 / Software: FastSeq for Windows Version 2.0b  
 / Current Application Date: 05/09/1999  
 / Filing Date: 05/09/1999  
 / Classification:  
 / Patent Classification:  
 / Application Number: 08/846,333  
 / Filing Date:  
 / Attorney/Agent Information:  
 / Name: Edwards, LLC  
 / Registration Number: 30,605  
 / Reference/Docket Number: 8389-0060-999  
 / Telecommunication Information:  
 / Telephone: 646-493-5555  
 / Telefax: 646-493-5555  
 / Telex: 6641 PENNIE  
 / Information For SEQ ID NO: 11:  
 / Sequence Characteristics:  
 / Length: 1205 amino acids  
 / Type: amino acid  
 / Strandedness: single  
 / Topology: linear  
 / US-09-491-522-11

Query Match 11.98, Score 918.5, DB 4, Length 1205;  
 Best Local Similarity 31.88, Prod. No. 1,2e-65;  
 Matches 254, Conservative 105, Mismatches 339, Indels 101, Gaps 32;  
 Qv 91 QGQBPQADQTHLHVAJFVGPACBA-QQDTRVYVTHLQAEILHDSLSAGAFV 149  
 Db 248 RMRPQADQTHLHVAJFVGPACBA-QQDTRVYVTHLQAEILHDSLSAGAFV 307  
 Qv 150 HLYQVLTLEPQADH-TANLUSLSLVGMSQ-TINPEQDTHQADLVIVTFDE 207  
 Db 308 VLVRLVLSVYKMSLITGQFSLNCEVLAQVQKQFDTQDTHV-DRAVITQDQF- 365  
 Qv 208 LFNQBVGVQVLQAGASCTWELCTEDQDQVLTQVLAHISGLQLEHDSAGSCP 267  
 Db 366 ---QFQMDQVAPVQMDQVRECTLEMDQFSAVVAHETGVKMDQ-QMRCD 421  
 Qv 268 S---QRYVASDGAAGLASCRRQLLSLAGACAWDPFQPSAGHPDAQ- 323  
 Db 422 EYRLSMAVQQAHPHPSRACQCEGLRYLS-----YQDQDPTFWHAPDAQ 475  
 Qv 324 POLYTSANQVAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAF 383  
 Db 476 POLYTSANQVAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAFQAF 533  
 Qv 384 GYEVKSKRGCSRLVETIAHVGMSGSRGSCGQVYVTRQCNPRAFQ 443  
 Db 534 AGRCCTFYGRQWLT--FDLAKGQMGMSPFQSGCTGQYVTRQCNPRAFQ 591  
 Qv 444 RACVADLQAGCTQLEPSCQACQDQFASFGSGAFYMGAAVHQQD 503  
 Db 592 RYCSGLQDQFQSCQDQADQFQEQDQD---LFFQDQD-HM---LFFQDQD 644  
 Qv 504 A--LCHMC--RATGSIKMGQDQFQDQDQDQDQDQDQDQDQDQDQDQDQD 559  
 Db 645 ALEXCHLYCEKGTGVYKMK--HMDQDQDQDQDQDQDQDQDQDQDQDQDQD 697  
 Qv 560 DQQWQD 618  
 Db 698 GSKQD 757  
 Qv 618 AYR--IGQYVAGMSISNT-TYPEL-----LEGRGVFVATLEDRPLEERI 668  
 Db 758 AYKLEQFGLFQD 802  
 Qv 669 MFL-----QEDADQVQRY-----GEYQNLTRFDITTFQFQDQWV 711  
 Db 803 MFLAGTTCVIVFQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 852  
 Qv 712 AAVR-GEVSCQAGLRWVNSCLQABKELVETVQCGQPPAFKCYLEPC-PPY 769  
 Db 912 ALKNSPQKQCGQSGQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 912  
 Qv 770 AYKQFQSCNQC-GLGRPBYCYE-AGSLKLTFFAPKACQAQAPAVALETCFQ 827  
 Db 913 VNTGWMFQSGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969  
 Qv 828 PCFARVNEVSESCSAGAGALANETVCVQALQLEAPVTEGSGVDSKLPAREFCV 846  
 Db 970 LCPJHMA-----GPN-----SCSCTCYTBEVFLDTA 988

RESULT 8  
 / Sequence 11, Application US/09445023A  
 / Patent No. 655588  
 / Applicant: Kunitaka  
 / Applicant: Kunitaka  
 / Applicant: Inoguchi, Eiji  
 / Applicant: Katozaki, Michinori  
 / Applicant: Katozaki, Michinori  
 / Applicant: Takeda, Yukio  
 / Applicant: Matsushima, Kouji  
 / Applicant: Kuno, Kouji



QY 708 ---AAVAVGSCVCGAGLAWVNSCLQAKELVETVCCSQSP--- 753  
 DB 848 STRAIPPTFAVTEI---GECCKCELG-N-----QRLVVECDING--OPAS 890  
 QY 754 ---PAMFEACVLECFPVYAGVGFQSGACCGGLALRVEVPCVAGQSLATLPA 806  
 DB 891 ECKNEVPEASTPCADHPC-FQMLGJGSGVQKQFQSGELKLSHGGVYL--- 943  
 QY 807 BCAGAGQQAQPAVALETQPCP 828  
 DB 944 ---SHSCDPLKCP 954  
 RESULT 10 559-2  
 US-09-369-364A-7  
 ; Sequence 2, Application US/0956959  
 ; Patent No. 6643377  
 ; GENERAL INFORMATION: Inventor: Robert A. Paul  
 ; APPLICANT: Allard, John  
 ; APPLICANT: Heller, Renu  
 ; APPLICANT: Van Wart, Harold  
 ; TITLE OF INVENTION: Composition Encoding the Same  
 ; FILE REFERENCE: US/09/568,559  
 ; CURRENT APPLICATION NUMBER: US/09/568,559  
 ; PRIOR APPLICATION NUMBER: 60/133,343  
 ; PRIOR FILING DATE: 1995-05-10  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: SEQ ID NOS: 1-4  
 ; SEQ ID NO 2: FASTSEQ for Windows Version 4.0  
 ; LENGTH: 949  
 ; ORGANISM: human  
 ; ORGANISM: human  
 US-09-569-559-2  
 Query Match 11.88; Score 812; DB 4; Length 949;  
 Local Similarity 29.78; Patent No. 2,8e-65;  
 Matches 238; Conservative 110; Mismatches 134; Gaps 31;  
 QY 813 PSEFGPGRQ-----RQBAAGGTLHLELVNVPVQAKQDTRVNLNCA 135  
 DB 213 PQALQGVGTGCTGKKEFVSHRYVLAQVQAGAFEGSLGHLTLTSTVA 272  
 QY 136 ELLEDELQAFQVPLQVLTDEGANTTANLSLVCSQSTNEDTQCPA 195  
 DB 272 RLYRFSFNSVGLVVLVHDEQCEVTSANLANTCNQKQNPDRBACH 332  
 QY 195 ELVYTFTELELPGNR--QVRVQVQAGCFNSCLTDEQDQTTAHELTCHP 253  
 DB 332 DIALTFQDL--CGSQDCTLQAVGVTCDEPSCSVIEDQGLQAFTHLGVF 389  
 QY 254 GLENDGAG--SCQCPGHWAS-----DGAAPAGLAFPCSEGLLSGARG 304  
 DB 390 NHQDCACASLVNQVHMAHMLNLDHCP-----NFCANVITFLDNGEC 444  
 QY 305 VQDPFCQCSAGRP--PDAQGVYANQCEVATPCVATVARENLQWALCSCH 361  
 DB 445 LMDQFC-----NPTQLGELPTGVANQCTFQESGKCPA--ASTGTLACT 494  
 QY 361 TQPLQSSCELLVLTQCEVNSKGRCHVLEL-----TPTAAVHNSWQPS 417  
 DB 495 GTSVGVVCTQTFPMATQSGGKCNKQVKNRKHQVDFPF--HSGVQWQPS 551  
 QY 418 PSESGVQVTFRECCQNPAPFGACVADLQAMQWQCAL--EKTQLQSCQCAT 476  
 DB 552 DSGATGGVQVTFRECCQNPAPFGACVADLQAMQWQCAL--EKTQLQSCQCAT 476  
 QY 477 DQPLLESGFAMFTHVAGVPHQDCA--LCHWQVGLGDSFIMKRGDFTQCTCP 533  
 DB 611 INFESASFGSGAPVW---TPKATGVSPURCKQLQMGVQVFLQKQVDTQCP 667

QY 534 SPREDOTLSVNGSCRTGFCGMRGQVMDQVQCDNSTSPKMSFTAGRAEY 593  
 DB 668 ---SST-ETCGGCGVADGACN110GSEKFNKQVQDNGSTCKEISGVTSAP-QY 720  
 QY 594 VTELVTPNTVETIANH---APLFTHAVRIG-GRVTVAGMDGSPNTTPSLGG 647  
 DB 721 HLIITFPQNTIEVQVQKGGNNGSFALMAKQDTLINDYDLS-----TLAQDI 774  
 QY 648 RVEVAVLATEDEKLEPRTIRWQIQAQDQVTVRQVGEVTPQITFTFQPKQ 707  
 DB 775 MKQVYVYEGSSNALEIRISFEPKEPITQVY-----TVGNALPKNITVVDKDS 829  
 QY 780 ---AMV---AAVVRQVSCVCGAGLAWVNSCLQAKELVETVCCSQSP--- 753  
 DB 838 SPNAIPPTFAVTEI---GECCKCELG-N-----QRLVVECDING--OPAS 872  
 QY 754 ---PAMFEACVLECFPVYAGVGFQSGACCGGLALRVEVPCVAGQSLATLPA 806  
 DB 873 ECKNEVPEASTPCADHPC-FQMLGJGSGVQKQFQSGELKLSHGGVYL--- 925  
 QY 807 BCAGAGQQAQPAVALETQPCP 828  
 DB 926 ---SHSCDPLKCP 936  
 RESULT 11  
 US-09-369-364A-7  
 ; Sequence 7, Application US/0956964A  
 ; Patent No. 6391620  
 ; GENERAL INFORMATION: Inventor: Robert A. Paul  
 ; APPLICANT: Apple, Sunee  
 ; APPLICANT: Harkainen, Tiina L.  
 ; APPLICANT: INVENTOR: N. Satomaa  
 ; FILE REFERENCE: 26473/4007/10-30-00  
 ; CURRENT APPLICATION NUMBER: US/09/369,364A  
 ; PRIOR APPLICATION NUMBER: 26473/4007/10-30-00  
 ; NUMBER OF SEQ NOS: 37  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 7: 1  
 ; LENGTH: 97  
 ; ORGANISM: Homo sapiens  
 ; ORGANISM: Homo sapiens ADAMTS-7  
 US-09-369-364A-7  
 Query Match 11.38; Score 864.5; DB 4; Length 997;  
 Local Similarity 29.38; Patent No. 2.2e-61;  
 Matches 275; Conservative 94; Mismatches 380; Indels 191; Gaps 36;  
 QY 17 LGLALMLHQRHAPRCPLC-----VAGLACQFLGCGPSPHQSCLQ 62  
 DB 116 LQRAHTRAH-----TPACILLGVQVPELEGGLALISACQAGVFLQN-EDITFI 166  
 QY 63 ALF-PQAVSSILSPQIKQRPSPGPR-----QQRQR 96  
 DB 167 PDAQAPRQAPRQAPRQAPRQAPRQAPRQAPRQAPRQAPRQAPRQAPRQAPRQ 226  
 QY 718 PQAGQGLH-----LELVVAGVPVQAH-DETERVYLVNIGALLRQSLQ 146  
 DB 227 RPLRRLHQRVSKRWCTVTVVAGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 286  
 QY 147 FRVLVQVVLVTEGANTANLTSLSVCSQSTNEDTQCPAHLVITRED 206  
 DB 287 IHTVTLVLEEDULKTHAQNTLAFSCQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 346  
 QY 287 ELDPGN--QVRVQVQAGCFNSCLTDEQDQTTAHELTCHP 253  
 DB 347 -CAMMRPCEZLISVQV 404  
 QY 265 QGSG--HMASDQAPAGLAFPCSEGLLSGARGVQVDPFQCPGACHPP 321  
 DB 405 CEVGRAPFTFMSQLVYQALPWRSCSNITFIDQWGLCGLDQPAKDIQF--PS 461



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US-09-369-364A-15
/ Sequence 15: Application US/09369364A
/ Patent No. 6416574
/ GENERAL INFORMATION:
/ APPLICANT: Apco, Suneei
/ APPLICANT: Burselstein, Tina L.
/ APPLICANT: Burselstein, Tina L.
/ TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
/ FILE REFERENCE: 26473/4007/10-30-00
/ CURRENT APPLICATION NUMBER: US/09369364A
/ INVENTION DATE: 1997-08-06
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NOS: 82
/ TYPE: PAT
/ ORGANISM: Mus musculus ADAMTS-9
/ US-09-369-364A-15

Query Watch
Best Local Similarity 30.8%; Seed No. 2,8e-57; Length 874;
Matches 242; Conservative 115; Mismatches 347; Indels 114; Gaps 27;

QY 105 LELVAFVDFQAGQDTERVLTNLTGAEELDSAGFVFLVQVLTPEGAR 164
DB 134 VEWVVAHVRVPRHGMQHLITLMTLIVSLVSGSLNIVLVVWLVNNGS 193
QY 145 NITANLSELSVCSNQTIN----FEDTDPGHADVLTIRLELDFPQSRVGTV 220
DB 194 YINFMATGTLNCKNHSVYLGSTQST-----AGVFRULGACRKTQTL 246
QY 181 NITANLSELSVCSNQTIN----FEDTDPGHADVLTIRLELDFPQSRVGTV 220
DB 221 LGAGCFNSMCLITFDGDLGVTAHESGSLFQEDGAPGSCFSG-----HNNAS 275
DB 247 LUTCDPFCSSISDSGUSTATATNHLGVNPHNDS--NKLSEVSVQFNAP 304
QY 276 GAAPFAGLAFCSGRQLSLSAGARCWDFPFGAGHCF--PDAGFGLYSANQC 334
DB 305 LNFVTFPMWMSCKNLTTFELVPSYSELN-----SPAKVTLLPQCLPVLNNG 360
QY 335 RVAFGEVACTFAEHLQMLQALSCHTDPLQSSCRLLVPLDITGQVEMSKRC 394
DB 361 ELTFPSGVQTPYAC-----DRLLKNVGNAGKACTQTFPAQTLCEPQKCFE 416
QY 395 RSLVETLVNAGWMSHSPSCRSRGGVVTTRQCNHPPAGACVQGLDQAR 454
DB 417 VRKEGEP--ALDGSNHSFPTQVLTGSLKTAHSCNPEPQACVLTGEMKEK 474
QY 455 MNTQACCKTQELPSQCAARTDQGLPAGSFGAFVHGAQVPHSQDAL--CHRM 511
DB 475 SCVTFQMKQDQFQACNPDGQFNTN--GLLSVYM-----PKYSGTLWCKL 530
QY 512 ALGDSYIMKSGDLDITTCVQREHGTSLGYSRCACTGCDMSQDMSQVQVC 571
DB 531 VAGNTVQLERDVLTITVC-----GQVMDLTVCLQCSCHLLNLSKWKVQ 584
QY 572 GDNSTSCFSGFSTAGAREVITFTVFNLTYSVIANRPLFT-----HLAV-RIG 623
DB 585 GDNSTSCVTAUTVNTVH-VQNVVTSVAGNSTDVQHS--FSQWSDNTALS 641
QY 624 GRVVAAGMSISPTTVPSELLEDQREVYV--ALTE-----DLRFLSEIRW 677
DB 642 RELLTLDQVYNS-----KREVGAGVATVSGSNV--CEBLNLTQISELL 689
QY 678 TQTRVAYREVQNTDPITFTV---FQPHRQM-----VMAVQSVSCGGLN 729
DB 690 LQVL-----SVQLWDFYFSPNITDQFQVWNSHGNQACEKQ-----GE 739
QY 730 WSCLDQARKEVETVQSGQPPMPFACVLECFCTFVYAGQVDFQVSNCSQGL 789
DB 740 KCLTRESQDVSQDCBLQFQVFALEGTQD--CLMRTVASKEGACQGLT 798
QY 790 KCTVCEAGSGSLTCTTPAPRACAGAQPAVALETCNFCQPCAR-----NE 837
DB 837

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QY 714 VAGFVSQAGLRWVNSCLOAKRELVTVOGSGQQPAPACVLEPC 765  
 DB 559 --GCKTCKGATKAGLKLKLSGCGSLSHS-SCPLAPKPTFDCTVAC 607  
 RESUR 13  
 : Sequence 24, Application US/0963791  
 : Patent No. 5649399  
 : ORIGINATOR INFORMATION: Gregory  
 : APPLICANT: Turner, C. Alexander Jr.  
 : APPLICANT: Friedrich, Glenn  
 : APPLICANT: Johnson, James  
 : APPLICANT: Seidman, Brian  
 : APPLICANT: Sands, Arthur T.  
 : TITLE OF INVENTION: No. 6449399el Human Proteases and Polynucleotides Encoding the Same  
 : CURRENT APPLICATION NUMBER: US/09/563,791  
 : CURRENT FILING DATE: 2000-12-08  
 : PRIOR APPLICATION NUMBER: US 60/169,769  
 : INVENTION PRIORITY DATE: 2000-12-09  
 : NUMBER OF SEQ ID NOS: 25  
 : SOFTWARE: FastSeq for Windows Version 4.0  
 : SEQ ID NO 24  
 : DEFINITION: Homo sapiens  
 : TYPE: EST  
 : ORGANISM: Homo sapiens  
 : US-09-563-791-24  
 Query Match 10.04; Score 776; DB 4; Length 757;  
 Best Local Similarity 29.94; Pred. No. 2,3e-54;  
 Matches 212; Conservative 106; Mismatches 283; Indels 109; Gaps 32;  
 QY 94 RQRAAGGILHLLVAVGVDFQAH-CEITERYVLNIGAILDPSLGAQFVHLV 152  
 DB 90 RQGSYSYEFVTLVADMMWVYQKDKIENYLSVAVLADSLGWNVIVA 49  
 QY 153 KWLVLTEPAGNITAN-LTSLSLVCHSGSOTI---NPEDOTDP---GADLALVTR 203  
 DB 150 LKLVLTEDQ--PLSLRHAAKSLDSFCFKKSLGSGKQNTIPKTAHQAHLVTR 107  
 QY 204 PDL---ELPDQRVGVYQAGAGSFTWCLTETFDLGTVAHIGFSGLEHGG 259  
 DB 200 YDICTYKKEGCS---TGLASVAVQCEPESKSIENHIGLGSATFAHILGRNFQHDG 264  
 QY 260 AGSGSGDPSCH---WASDAQAFAGLAWGFSRGLLSLSAGTACVADPPDPQS 315  
 DB 265 I-GNSGCKEBAKAAKAAHTANTHPSWAKSADYTSFDSGSGTLNRP---PGR 320  
 QY 316 RHPPFPAQGLYTSANQCRVAFQVAVCTFAHSLHWQAALSCHTDPLQGS-CEBLL 374  
 DB 321 DPLTPAVAHVQADQACRCPATGATSGCKTG---EYCKELAC---LKSANVYNS 372  
 QY 375 VFLQGTQC---GVKK-WCSGSGSLVELFPIA---AVHGRMSNGPSKSGCG 426  
 DB 373 IPAAEGLTQGNIEKWCYQDC-----VPTGFWISDGGMGSLMWSKSGTGG 426  
 QY 427 VYTRRQNNPFAFGACVAGDLQAMQTCACQLFEMSGQCAHQQPISLSEFG 486  
 DB 427 VSSLSARCCFATSGAGGKGLAEKRYKSNQCPGLASGAFREKQCAUFNMFR 482  
 QY 487 GASFYHGAAGVHSGQAL-CEHMCRAIGESFMGDSFLQTCRVFSQPDOTSLC 545  
 DB 483 -GYTHM---KYPTGGVYFCAKCLABSTNHYTERKAPVLDTC-----NAUSLDC 532  
 QY 546 VSGSKATPGCDGMSGQVWRQVCGDNSTCSFSGSFTAGAR-EYVTFVLYTNLT 604  
 DB 533 INDCGNGCNMILSDADEKRCVCGDSTCAIEGFPNCSLPGSGHVFYPRGV 592  
 QY 605 SVYIANRPLFTHAVRI-GRVYVAGNGISNTYTFSLSDGVERVVALTEDRLPL 663

DB 593 HIEVREVMNIALKSEDDYINGAWTD----WPKFQVAGTAFHYKPTDEPESL 648  
 QY 664 BEIRIWGLODADIVY--RAYEBSG---NCTP-----DITFHYQKFPQAKMA 712  
 DB 649 EAL--GPTSLNVLWLLQBNLAITFYNFVITTSQDNVEQFTM-----NQPM--- 698  
 QY 713 AVRGSCYVSGAG-----LKNVNSCLDA---KRELVTVOG 748  
 DB 699 ---SECATCAGDNPTQPTQBARAKTWLLISVALCLAKLIGNISCH 744  
 Search completed: March 13, 2004, 07:46:05  
 Job time : 64.7375 secs



GenCore version 5.1.6  
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OW protein - protein search, using sw model  
Run on: March 13, 2004, 07:33:19 ; Search time 3.3849 seconds  
(without alignments)  
2756-533 Mammalian cell updates/sec

Title: US-09-836-712-2\_COPY\_1\_97  
Perfect score: 534  
Sequence: 1 PQRTPFAFHSAPLQALA.....FLKGRPFQQRQQR 97  
Scoring table: BLOSUM42  
Gapop 10.0 , Gapext 0.5

Searched: 231366 seqs, 96191526 residues  
Total number of hits satisfying chosen parameters: 281366

Minimum DB seq length: 8  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 08  
Minimum E-Value: 1E-06  
Listing first 49 summaries

Database : PIR78:  
1: PIR78  
2: PIR2  
3: PIR3  
4: PIR4

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	79.5	14.9	333	2	JC4875	zinc-finger protei
2	74.5	14.0	237	2	T40577	probate phosphat
3	73.5	13.9	250	2	U04496	tyrosine kinase re
4	74	13.9	510	2	A53117	tyrosine kinase re
5	73.5	13.8	67	2	AG2114	hypothetical prote
6	72.5	13.5	402	2	U04503	connexin44 - bovin
7	72	13.5	402	2	U04503	connexin44 - bovin
8	71.5	13.4	837	2	A57542	p56 protein - mous
9	71	13.3	913	2	A48240	receptor tyrosine
10	70.5	13.2	135	2	U04384	hypothetical prote
11	70.5	13.2	135	2	U04384	hypothetical prote
12	70.5	13.2	771	2	B38282	granulocyte colony
13	70	13.1	533	1	J02486	activin receptor I
14	70	13.1	513	2	A39896	activin receptor I
15	70	13.1	513	2	A39896	activin receptor I
16	70	13.1	513	2	B23288	activin receptor t
17	70	13.1	513	2	U45950	activin receptor t
18	69	12.9	209	2	A57544	hypothetical prote
19	69	12.9	209	2	A57544	hypothetical prote
20	69	12.9	535	2	T11212	hypothetical prote
21	69	12.9	920	2	B34493	collagen alpha 1(I
22	68.5	12.9	920	2	B34493	collagen alpha 1(I
23	68.5	12.9	1074	2	T24897	hypothetical prote
24	68.5	12.9	1074	2	T24897	hypothetical prote
25	68	12.7	300	2	T74482	hypothetical prote
26	68	12.7	300	2	T74482	hypothetical prote
27	68	12.7	501	2	BV8MCA	mycolysin IEC 1.4
28	68	12.7	501	2	BV8MCA	mycolysin IEC 1.4
29	68	12.7	2783	2	A41948	phosphatase regu
30	67.5	12.6	331	2	T40577	regulatory protein
31	67.5	12.6	499	2	B09880	hypothetical prote

## ALIGNMENTS

## RESULT 1

zinc-finger protein Zic4 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 15-Aug-1996 sequence, revision 18-Oct-1996 #text\_change 05-Nov-1999  
S:Accession: U04875, MIM:362832; PMID:682319  
S:Author: Yon, A.; Hayashizaki, Y.; Okazaki, Y.; Chapman, V.M.; Mikohiba, K.  
Gene 112, 231-234, 1996  
Article: Identification and characterization of Zic4, a new member of the mouse Zic gene  
A:Accession: U04875  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Cross-references: DBJ:J78174; NID:G1480004; PIN:EM11240.1; PID:d011902; PID:G148  
C:Genetics:  
A:Gene: Zic4  
A:Map: Chromosome 9  
C:Keywords: zinc finger  
F:119-298/Region: zinc fingers

Query March 14-91, Score 79.5, DB 2, Length 353,  
Best Local Similarity 27.9%, Read No. 1.33

Matches 31; Conservative 12; Mismatches 49; Indels 19; Gaps 4;  
QY 1 PQRTPFAFHSAPLQALAL-----RMGRH-----PACCPFLVAGIACGP---46  
DB 51 PQRTPFAFHSAPLQALALRDPMTARSEFPAPGARDLATALR-GYGNK 109  
QY 47 -----LACQPSHFQSCALQEPASVPCALKGRPFQPCQQRQ 93  
DB 210 LKQNLATPAGCAFFATWQPIKQELICMLQDCDSMPSPKCTFTFMH 160

## RESULT 2

740577  
probate phosphatidylinositol 3-kinase - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Sep-1999 sequence, revision 15-Sep-2000 #text\_change 06-Oct-2000  
S:Accession: T3913, T40577  
S:Author: Kishimoto, A.; Sarrell, B.G.; Oliver, K.; Harris, D.  
A:Reference number: 221890  
A:Reference number: 221890  
A:Accession: T3913  
A:Molecule type: DNA  
A:Cross-references: EMBL:AL049558; PIR:G040167.1; GSPDB:GNO0057, SPDB:SPFEC16.07c  
A:Status: nucleic acid sequence not shown  
A:Cross-references: EMBL:AL049558; PIR:G040167.1; GSPDB:GNO0057, SPDB:SPFEC16.07c  
A:Map: Chromosome 1; Submitted to the EMBL Data Library, January 1996  
A:Reference number: 221938  
A:Accession: T40577

A>Status: preliminary; translated from GB/EWEL/DBDZ  
 A.Molecule type: RNA  
 A.CSpecies: Rattus sp. (rat)  
 A.Cross-references: EMBL:U035216; PIDN:CA22805.1; GSPDB:GN00067; SPOB:SPB644.01c  
 A.Experimental source: strain 972H-4; cosmid 646  
 A.Genetic position: 2  
 A.Map position: 2  
 C/Superfamily: yeast TOR2 protein

Query Match 14.0%; Score 74.5; DB 2; Length 2337;  
 Best Local Similarity 29.9%; Pred. No. 23;  
 Matches 20; Conservative 10; Mismatches 28; Indels 9; Gaps 3;  
 QY 17 LGALHWHQHPHRCPCPLCA-----GLACGLGCGP--SHFQSCQLALQEPQ 68  
 DB 1337 LGVALHRSFSLHQAALAAVQAQVADLFAHMF-VSCNEDYHGFELHWSFSL 1195  
 QY 69 VSTSLP 75  
 DB 1156 TSPHSP 1202

RESULT 3  
 180329 for tyrosine kinase - rat (fragment)  
 CSpecies: Rattus sp. (rat)  
 C.Date: 02-Aug-1996 [sequence\_revision 02-Aug-1996 #ext\_change 24-Sep-1999  
 A.Accession: 180329 H; Ijichi, A.; Tofilon, P.J.  
 A.Reference number: 180329  
 A.Molecule type: RNA  
 A.Status: preliminary; translated from GB/EWEL/DBDZ  
 A.Experimental source: strain 972H-4; cosmid 646  
 A.Genetic position: 2  
 A.Map position: 2  
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 13.9%; Score 74; DB 2; Length 220;  
 Best Local Similarity 29.6%; Pred. No. 2; 3;  
 Matches 29; Conservative 9; Mismatches 28; Indels 32; Gaps 6;  
 QY 1 PGRTPPK-APSHAPLL--GLA-----LLEHWHQHPHRCPCPLCAVGLACGF 47  
 DB 80 PGRTPPKPTPHNCTPNSVGNLSLNPVALLATYAPPGPDP----- 127  
 QY 48 LQWQ-PSHQSCQLALQEPQVSTSLPAGLGRPP 84  
 DB 128 TPAAKATPTQACSDYMEP-----KQGLPLPPP 159

RESULT 4  
 16053  
 CSpecies: Bos primigenius taurus (cattle)  
 C.Date: 16-Aug-1996 [sequence\_revision 16-Aug-1996 #ext\_change 13-Aug-1999  
 A.Accession: 16053  
 A.Reference number: 16053  
 A.Molecule type: RNA  
 A.Status: preliminary; translated from GB/EWEL/DBDZ  
 A.Experimental source: strain 972H-4; cosmid 646  
 A.Genetic position: 2  
 A.Map position: 2  
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoindin I amino-ter

C/Keywords: ATP, discoidin I amino-terminal homology <DB>  
 F:601-909/Domain: protein kinase homology <DB>  
 F:611-621/Region: protein kinase ATP-binding motif

Query Match 13.9%; Score 74; DB 2; Length 910;  
 Best Local Similarity 29.6%; Pred. No. 11;  
 Matches 29; Conservative 9; Mismatches 28; Indels 32; Gaps 6;  
 QY 1 PGRTPPK-APSHAPLL--GLA-----LLEHWHQHPHRCPCPLCAVGLACGF 47  
 DB 480 PGRTPPKPTPHNCTPNSVGNLSLNPVALLATYAPPGPDP----- 527  
 QY 48 LQWQ-PSHQSCQLALQEPQVSTSLPAGLGRPP 84  
 DB 528 TPAAKATPTQACSDYMEP-----KQGLPLPPP 555

RESULT 5  
 AG214  
 A.Molecule type: RNA  
 A.CSpecies: Nostoc sp. (strain PCC 7120)  
 A.Name: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C.Date: 14-Dec-2001 [sequence\_revision 14-Dec-2001 #ext\_change 09-Dec-2002  
 C.Date: 14-Dec-2001  
 A.Accession: AG214  
 A.Reference number: AG214  
 A.Molecule type: RNA  
 A.Status: preliminary; translated from GB/EWEL/DBDZ  
 A.Experimental source: strain PCC 7120  
 A.Genetic position: 2  
 A.Map position: 2  
 C/Superfamily: conserved hypothetical protein sll033; conserved hypothetical protein

Query Match 13.9%; Score 73.5; DB 2; Length 647;  
 Best Local Similarity 34.5%; Pred. No. 8.9;  
 Matches 29; Conservative 23; Mismatches 23; Indels 25; Gaps 7;  
 QY 7 PAPSHPAPLLGALLHWHQHPHRCPCPLCAVGLACGF-----GSLTLCG--QPSHPQ 58  
 DB 581 PAPSHPAPLLGALLHWHQHPHRCPCPLCAVGLACGF-----GSLTLCG--QPSHPQ 629  
 QY 59 SCQLALQEPQVSTSLPAGLGR 82  
 DB 630 MC-QDL-PFSYQVCSPP---RGR 647

RESULT 6  
 16053  
 CSpecies: Bos primigenius taurus (cattle)  
 C.Date: 16-Aug-1996 [sequence\_revision 16-Aug-1996 #ext\_change 13-Aug-1999  
 A.Accession: 16053  
 A.Reference number: 16053  
 A.Molecule type: RNA  
 A.Status: preliminary; translated from GB/EWEL/DBDZ  
 A.Experimental source: strain 972H-4; cosmid 646  
 A.Genetic position: 2  
 A.Map position: 2  
 C/Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoindin I amino-ter

Query Match 13.9%; Score 72; DB 2; Length 402;  
 Best Local Similarity 30.9%; Pred. No. 8.1;  
 Matches 21; Conservative 6; Mismatches 27; Indels 16; Gaps 1;





```

A:Reference number: A39896; MUID:91256317; PMID:164680
A:Accession: A39896
A:Species: Rattus norvegicus
A:Molecule type: mRNA
A:Residues: 1-513 <MAT>
A:Source: M6997, NID, g1463; F050, M6931, 1, PTD, g191664
C:Source reference: 1; protein kinase homology
C:Keywords: ATP; receptor; sarine/threonine-specific protein kinase; transmembrane prote
F:190-486/Domain: protein kinase homology <KIN>

Query Match      13.1%  Score 70; DB 2; Length 513;
Best Local Similarity 27.7%  P-Id. No. 16;
Matches 23; Conservative 7; Mismatches 27; Indels 26; Gaps 4;

QY 4 FTTPKAPNSHAPLGLALLMQRPRAPCPPLCVAGILACGLQWGSFHSQCLOA 63
DB 129 VTKPTPTILLISLV-----PLMLGIVICAF---MYTHRMAYPPV 171
QY 64 LEPQVNSYLSGAPLKGPPSP 86
DB 172 LVFTQ-----DQGP-----PSP 185

RESULT 15
A49393; activin receptor Acrb1 - rat (fragment)
A:Reference number: A49393; MUID:93279247; PMID:951668
A:Accession: A49393
A:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #tax_change 23-May-1997
C:Accession: A49393, M.B.: Chem. C.L.
Endocrinology 132, 2593-2600, 1993
A:Title: Expression of type II activin receptor genes in the male and female reproductiv
A:Reference number: A49393; MUID:93279247; PMID:951668
A:Accession: A49393
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-513 <MAT>
A:Source: M6997, NID, g1463; F050, M6931, 1, PTD, g191664
C:Source reference: 1; protein kinase homology
C:Superfamily: activin receptor II; protein kinase homology
C:Keywords: ATP; receptor
F:190-486/Domain: protein kinase homology <KIN>

Query Match      13.1%  Score 70; DB 2; Length 513;
Best Local Similarity 27.7%  P-Id. No. 16;
Matches 23; Conservative 7; Mismatches 27; Indels 26; Gaps 4;

QY 4 FTTPKAPNSHAPLGLALLMQRPRAPCPPLCVAGILACGLQWGSFHSQCLOA 63
DB 129 VTKPTPTILLISLV-----PLMLGIVICAF---MYTHRMAYPPV 171
QY 64 LEPQVNSYLSGAPLKGPPSP 86
DB 172 LVFTQ-----DQGP-----PSP 185

Search completed: March 13, 2004, 07:44:38
CPU time : 5.3643 secs

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[illegible]



Query March 14.0%; Score 74.5; DB 1: Length 2337;  
Best Local Similarity 29.9%; Pres. No. 20;  
Matches 20; Conservative 10; Mismatches 28; Indels 9; Gaps 3;  
QY 17 LGALRLKQHPHRCPPCLCA-----GLAGCLQNGPQ--SHFGSCGLAQLPCA 68  
DB 1137 LGVLLRSEFSLKACAAALAAAYQPLADFNASF-VSNSELYDFHDEELVSTETAL 1195  
QY 69 VSTHSP 75  
DB 1196 TSHHSP 1202  
RESULT 4  
DRI: RPT: PAT: STANDB: PRT: 910 AA.  
AC Q63474;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-2007 (Rel. 45, Last sequence update)  
DT 01-NOV-2007 (Rel. 45, Last sequence update)  
DE Epithelial discoidin domain receptor 1 precursor (EC 2.7.1.112)  
DE (Tyrosine kinase DOR) (Discoidin receptor tyrosine kinase) (Tyrosine-  
DE protein kinase CKM) (Cell adhesion kinase) (Protein-tyrosine kinase)  
DE DRI or EDRI or PTK3  
OS Rattus norvegicus (Rat).  
GN Karyokinas; Reptarata; Chordata; Craniata; Vertebrata; Eumetazoa;  
OC Metazoa; Eumetazoa; Reptarata; Chordata; Craniata; Vertebrata;  
OC NCBI\_TaxID=10116;  
[1]  
[1] SOURCE FROM N.A.  
[1] MEDLINE=3417930; PubMed=5127887;  
RA Sanchez M.P., Tapley P., Salvi S.S., He B., Pulido D., Barbedid M.;  
RT Isolation of Ptk3 protein kinases at the periphery of the developing  
RT of the developing brain.;  
RL Proc. Natl. Acad. Sci. U.S.A. 91:1819-1821(1994)  
CC 1- RECOGNITION BY SIMILARITY  
CC 1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC 1- TISSUE SPECIFICITY: Type I membrane protein.  
CC 1- TISSUE SPECIFICITY: Various embryonic and adult tissues; also  
CC proliferative zones of the developing brain; hippocampal neurons.  
CC 1- SIMILARITY: Belongs to the Tyr family of protein kinases. Inulin  
CC 1- SIMILARITY: Contains 1 P5/8 type C domain.  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)  
DB EMBL; Accession: A021089.1;  
DB HSP; Accession: P05833; SPTK.  
DR InterPro: IP0000421; FAS\_C  
DR InterPro: IP000819; GAF\_Kinase\_Like  
DR InterPro: IP0002021; ReceptorKinase  
DR InterPro: IP0001245; Tyr\_Kinase  
DR Pfam: PF00780; GAF\_Kinase\_Like  
DR Pfam: PF00066; Pkinase\_I  
DR PRINTS: P00109; TYR\_KINASE  
DR SMART: SM00301; FAS\_C\_Kinase; 1.  
DR SMART: SM00319; TyrcK; 1.  
DR PROSITE: PS0285; FAS\_C; 1.  
DR PROSITE: PS0285; FAS\_C; 1.

DR PROSITE: PS0286; FAS\_C; 1.  
DR PROSITE: PS0022; PAS\_C; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_CW; 1.  
DR PROSITE: PS0033; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS0033; RECEPTOR\_TYR\_KIN\_1; 1.  
KM Transferrin; Tyrosine-protein kinase; Glycoprotein; Signal;  
KM Phosphorylation; Transmembrane protein; Potential; ATP-binding;  
FT CHAIN 20 910  
FT DOMAIN 20 413  
FT DOMAIN 413 441  
FT DOMAIN 441 500  
FT DOMAIN 500 532  
FT DOMAIN 532 566  
FT DOMAIN 566 598  
FT DOMAIN 598 632  
FT NP\_BIND 632 651  
FT BINDING 652 682  
FT BINDING 682 712  
FT DISULFID 712 732  
FT MOD\_RES 510 510  
FT MOD\_RES 789 789  
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FT MOD\_RES 789 789  
FT CAZEHOD 212 212  
FT CAZEHOD 261 261  
FT CAZEHOD 351 351  
FT CAZEHOD 351 351  
QY 48 LOGKQ-PSHFQSCGLQHPQAVSVYAPGALGPP 84  
DB 480 PVRPRFQRTTHSACVPMGSLGALLNAPVLLATVAPPGPP 47  
QY 48 LOGKQ-PSHFQSCGLQHPQAVSVYAPGALGPP 84  
DB 528 TPANRKTPTQACGDYNEP-----KSGAPLPPPP 559  
RESULT 5  
DRI: RPT: PAT: STANDB: PRT: 325 AA.  
AC Q63474;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 26-FEB-2003 (Rel. 41, Last sequence update)  
DT 13-MAR-2004 (Rel. 42, Last annotation update)  
DE Epithelial discoidin domain receptor 1 precursor  
DE (Tyrosine kinase DOR) (Discoidin receptor tyrosine kinase) (Tyrosine-  
DE protein kinase CKM) (Cell adhesion kinase) (Protein-tyrosine kinase)  
DE DRI or EDRI or PTK3  
OS Rattus norvegicus (Rat).  
GN Karyokinas; Reptarata; Chordata; Craniata; Vertebrata; Eumetazoa;  
OC Metazoa; Eumetazoa; Reptarata; Chordata; Craniata; Vertebrata;  
OC NCBI\_TaxID=10116;  
[1]  
[1] SOURCE FROM N.A.  
[1] MEDLINE=3417930; PubMed=5127887;  
RA Sanchez M.P., Tapley P., Salvi S.S., He B., Pulido D., Barbedid M.;  
RT Isolation of Ptk3 protein kinases at the periphery of the developing  
RT of the developing brain.;  
RL Proc. Natl. Acad. Sci. U.S.A. 91:1819-1821(1994)  
CC 1- RECOGNITION BY SIMILARITY  
CC 1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC 1- TISSUE SPECIFICITY: Type I membrane protein.  
CC 1- TISSUE SPECIFICITY: Various embryonic and adult tissues; also  
CC proliferative zones of the developing brain; hippocampal neurons.  
CC 1- SIMILARITY: Belongs to the Tyr family of protein kinases. Inulin  
CC 1- SIMILARITY: Contains 1 P5/8 type C domain.  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)  
DB EMBL; Accession: A021089.1;  
DB HSP; Accession: P05833; SPTK.  
DR InterPro: IP0000421; FAS\_C  
DR InterPro: IP000819; GAF\_Kinase\_Like  
DR InterPro: IP0002021; ReceptorKinase  
DR InterPro: IP0001245; Tyr\_Kinase  
DR Pfam: PF00780; GAF\_Kinase\_Like  
DR Pfam: PF00066; Pkinase\_I  
DR PRINTS: P00109; TYR\_KINASE  
DR SMART: SM00301; FAS\_C\_Kinase; 1.  
DR SMART: SM00319; TyrcK; 1.  
DR PROSITE: PS0285; FAS\_C; 1.  
DR PROSITE: PS0285; FAS\_C; 1.







[illegible]

FT DOMAIN 31 465 TV/S PRO-CH  
FT DOMAIN 377 415 GLY/PRO-RICH  
FT DOMAIN 476 601 GLY/PRO-RICH  
FT DOMAIN 610 905 PROTEIN KINASE  
FT BINDING 655 655 ATP (BY SIMILARITY)  
Query Match 13.3%; Score 71; DB 1; Length 913;  
Local Similarity 6; Mismatches 29; Identifiers 32; Gaps 6;  
Query 1 PGRTTPKA-PSHSAPLL-GLA-----LIRQQRHFRACPLCTAGIACGL 47  
483 PVEPRGPNFSAACVNGSALLNPVALLATVAFVPGCPP----- 530  
DB 49 LOGQ-PHQSCQALQFPAVSTYSFAPLGRFP 84  
DB 531 TPANAFNTQAVSGDMFE-----KCAPLPPPEP 562  
RESULT 10  
THAT HUMAN  
ID THAS HUMAN STANDARD; PRT; 274 AA.  
CD CDS027; CDS027; 42, Created!  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DR THAS domain protein 9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OC NCBI-TaxID:9606;  
RN [1]-TaxID:9606;  
RP SEQUENCE FROM N.A.  
RC LocusPart; Vanehori K., Yoshida M., Kawanabe S., Ishida S., Ono Y.,  
RC Hotta T., Hiroaka S., Murakawa K., Takiguchi S., Kusano J.,  
RC Matenabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,  
RC Yamamoto Y., Inoue Y., Kawai-Hiro Y., Saito M., Nishikawa M., S.,  
RC Kimura K., Matsuo Y., Nakamura Y., Sekine M., Kiuchi H., Kanda K.,  
RC Nagatsuma M., Takahashi-Fujii A., Ohtsuka A., Sugiyama A., Kawakami B.,  
RC "NEO human cDNA sequencing project" Masuho Y., Nagai K., Isegai T.;  
RC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RL -1- SIMILARITY: Contains 1 THAP domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).)  
DR EMBL; AK057453; BAB11493.1;  
DR EMBL; AK057453; BAB14034.1;  
DR Genbank; BC023291; THAP8.  
DR EMBL; AK057453; BAB14034.1;  
DR Pfam; PF05485; THAP; 1; DMO.  
DR SMART; SM00692; DMO; 1.  
DR DMO; 1; DMO; 1.  
FT 2N FING 5 61 THAP  
FT 2N FING 5 61 THAP-TYPE  
FT CONFLICT 185 185 R -> Q (IN REF. 1; BAB71493).  
FT CONFLICT 185 185 R -> Q (IN REF. 1; BAB71493).  
FT CONFLICT 274 274 EDS020924566A1; CDS027.  
SQ SEQUENCE 274 AA, 30081 MW, EDS020924566A1; CDS027.  
Query Match 13.2%; Score 70.5; DB 1; Length 274;  
Local Similarity 2; Mismatches 15; Identifiers 27; Gaps 4;  
Matches 29; Conservative 2; Identifiers 27; Gaps 4;

QY 48 LDC-NHOS-----HFQSCQ-----ALFPAVSTYSFPAVSTYSF 82  
DB 44 MCHHWTFPSQHCLSEHFPSFQRMWVYLPQAVPSFSPGPAQSGRTSTQKE 103  
QY 83 -RPP 86  
DB 104 VSPPEP 109  
RESULT 11  
NQOC-THETH  
ID NQOC-THETH STANDARD; PRT; 606 AA.  
CD C1-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DR NQOC-THETH 12 (EC 1.6.9.5) NADH dehydrogenase  
DR 1, chain 12) (NON-1, chain 12).  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC NCBI-TaxID:274;  
RN [1]-TaxID:274;  
RP SEQUENCE FROM N.A.  
RC STEIN-HBS / ATCC 27634;  
RC MEDLINE-9717490; PubMed-9020134;  
EA Wang T., Chu S., Steinhilber N., NADH dehydrogenase (NQOC-1) of  
EA thermophilic bacterium Thermus thermophilus HB-8. Complete DNA  
EA sequence of the gene cluster and thermoelastic properties of the  
EA expressed NQOC2 subunit-1-4211 (1997).  
RC [1]-FUNCTION: NQOC-1 shuttles electrons from NADH, via FMN and iron-  
RC sulfur (Fe-S) centers, to quinones in the respiratory chain. The  
RC reduced electron acceptor quinone may then couple the redox reaction to proton  
RC translocation (for every two electrons transferred, four hydrogen  
RC ions are translocated across the cytoplasmic membrane), and thus  
RC constitute the MEMBRANE SECTOR OF THE COMPLEX.  
CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.  
CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNIT NQOC-14  
CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.  
CC -1- SIMILARITY: TO POLYPEPTIDE 5 OF THE NADH-UBINOL OXIDOREDUCTASE  
CC OF CHLOROPLASTS OR MITOCHONDRIA.  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk).)  
DR EMBL; U05050; BAB77493.1;  
DR PIR; T11309; T11309; NADH-UBINOL OXIDOREDUCTASE.  
DR InterPro; IPR001916; NADH-UBINOL OXIDOREDUCTASE.  
DR InterPro; IPR001750; Oxidized q1 + N.  
DR Pfam; PF00361; oxidized q1 + N.  
DR Pfam; PF00662; oxidized q1 + N. 1.  
DR PROSITE; PROSITE; NADH-UBINOL OXIDOREDUCTASE.  
DR TRANSXEN 29 49 POTENTIAL.  
DR TRANSXEN 29 49 POTENTIAL.  
DR TRANSXEN 104 126 POTENTIAL.  
DR TRANSXEN 126 146 POTENTIAL.  
DR TRANSXEN 165 185 POTENTIAL.  
DR TRANSXEN 185 206 POTENTIAL.  
DR TRANSXEN 206 226 POTENTIAL.  
DR TRANSXEN 226 246 POTENTIAL.  
DR TRANSXEN 246 266 POTENTIAL.  
DR TRANSXEN 266 286 POTENTIAL.













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FT CHAIN 75 1427 VON WILLEBRAND FACTOR-CLEANING PROTEASE.
SQ SEQUENCE 1427 AA; 153632 MW; 5B1C3A8C1A4442 CRC64;

Query Match
Best Local Similarity 77.5%; Score 414; DB 4; Length 1427;
Matches 74; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 MQUHPEALCPCCVAGIACGLFQCHQSHFQSCGLAPFVAVSYLSPAPLKRE 83
DB 1 MQUHPEALCPCCVAGIACGLFQCHQSHFQSCGLAPFVAVSYLSPAPLKRE 60

QY 84 PPSFQRCQRCQR 97
DB 63 PPSFQRCQRCQR 74

RESULT 2
ID Q9BYE0 PRELIMINARY; PRT; 225 AA.
AC Q9BYE0 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB BLH factor Hsf7.
CC Hsf7, hsp70 (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Butheria; Primates; Catarrhini; Hominiidae; Homo.
CC Hs11-taxid=9606;
PP SEQUENCE FROM N.A.
RX MEDJUNE-2160566; PubMed-1160262;
RA Hs70_X; PubMed-1160566; G. Sakata R.; Kageyama R.;
RT the presenilin-1 gene. This gene regulated by Notch and expressed in
RL Genes Cells 6:175-185(2001)
CC -1- TRANSCRIPTION FACTORS
DB ENBL; ABC49064; BAI3525.1; -.
DR Gene; HNCI15397; HSF7.
DR GO; GO:0013677; P-RNA binding; NAS.
DR GO; GO:0007498; P-mesoderm development; NAS.
DR GO; GO:0007498; P-mesoderm development; NAS.
DR InterPro; IPRO01092; HLH_Basic.
DR SMART; SM00351; HLH; 1.
DR PROSITE; PS00038; HLH; 1.
DR PROSITE; PS50888; HLH2.1.
PP SEQUENCE 235 AA; 24899 MW; 027553A8AC247 CRC64;

Query Match
Best Local Similarity 17.9%; Score 95.5; DB 4; Length 235;
Matches 34; Conservative 1; Mismatches 35; Indels 35; Gaps 5;

QY 130 PPRKPVDPFRPAPLAPALAPLPPPRHQQAPKAPLPPPPA 173
DB 130 PPRKPVDPFRPAPLAPALAPLPPPRHQQAPKAPLPPPPA 173

QY 50 CWP-SHFQSCQALQEPQVNSYLSIP-----GALPKGRPPSPOR 90
DB 174 ANWELCPDAGSGAPALPGLPPLPPPRHQQAPKAPLPPPPA 222

RESULT 3
ID Q9BK72 PRELIMINARY; PRT; 225 AA.
AC Q9BK72 2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB BLH factor Hsf7.
CC Hsf7, hsp70 (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SQ SEQUENCE 225 AA; 24869 MW; 4B22E7D7A7FF5E8 CRC64;

Query Match
Best Local Similarity 16.0%; Score 85.5; DB 11; Length 225;
Matches 33; Conservative 6; Mismatches 37; Indels 23; Gaps 6;

QY 1 PPRTRPAP-SHAPLGLALLHQRHPRAPLCPVAGIACGLQCHQSHFQSC 59
DB 136 PULPA-PPRTPDASGLPDLN---KRRPFWOCPF---SRLLA-----MSHQSRS 193

QY 60 C-----LQALPSVSYLSPAPLKGRPPSPOR 90
DB 184 AGSGAPAFNGLLPPLPPPRHQQAPKAPLPPPPA 222

RESULT 4
ID Q9JAG PRELIMINARY; PRT; 225 AA.
AC Q9JAG 09-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB BLH factor Hsf7.
CC Hsf7, hsp70 (Human).
CC Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC Hs11-taxid=9606;
PP SEQUENCE FROM N.A.
RA Hs70_X; PubMed-1160566; G. Sakata R.; Kageyama R.;
RT the presenilin-1 gene. This gene regulated by Notch and expressed in
RL Genes Cells 6:175-185(2001)
CC -1- TRANSCRIPTION FACTORS
DB ENBL; ABC49064; BAI3525.1; -.
DR Gene; HNCI15397; HSF7.
DR GO; GO:0013677; P-RNA binding; NAS.
DR GO; GO:0007498; P-mesoderm development; NAS.
DR GO; GO:0007498; P-mesoderm development; NAS.
DR InterPro; IPRO01092; HLH_Basic.
DR SMART; SM00351; HLH; 1.
DR PROSITE; PS00038; HLH; 1.
DR PROSITE; PS50888; HLH2.1.
PP SEQUENCE 235 AA; 24899 MW; 4B22E7D7A7FF5E8 CRC64;

Query Match
Best Local Similarity 15.8%; Score 84.5; DB 11; Length 225;
Matches 33; Conservative 6; Mismatches 37; Indels 23; Gaps 6;

```

Best Local Similarity 33.3%; Pred. No. 0.17;  
 Matches 33; Conservative 37; Mismatches 37; Indels 23; Gaps 6;  
 QY 1 PGRTPAP--SHAPLIGALLMGHPRACPCVUGLACGLACGKNSHFQSS 59  
 DB 139 KQLA--PPPLDAPFLDAPL-----HQPVPHQPP-----SPRLA-----KPSICSSR 183  
 QY 60 C-----IQALEPQVSYLSGAPKGRPSGQGR 90  
 DB 184 AGDSGAPATVGLPPPPPPVQCGAPKAPVAPPAHW 222

RESULT 5  
 ID Q8H468 PRELIMINARY; PRT; 281 AA.  
 AC Q8H468-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE P047001.26 protein.  
 OS Craya sativa (Isoponia cultivar-group).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Eriocaulaceae; Oryzaceae; Oryza.  
 NX NCBI\_TaxID:33947.  
 RN [1] \_SEQUENCE FROM N.A.  
 RP SOURCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Yanamoto K.,  
 RA "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 7, PAC  
 ST Clone:PM410D12-2001) to the EMBL/GenBank/DBJ databases.  
 RT EMBL; AF004300; BAC15992.1; --  
 EQ SEQUENCE 281 AA; 32264 MW; 3B2M33828FDFD732 CRC64;

Query Match 15.4%; Score 82.5; DB 10; Length 281;  
 Best Local Similarity 28.8%; Pred. No. 0.36;  
 Matches 36; Conservative 7; Mismatches 39; Indels 43; Gaps 6;  
 QY 1 PGRTPPAP-----SHAPLIGALLMGHPRACPCVUGLACGLFLOOW 51  
 DB 31 PMLPDEPAPAAAGASHTGSHGAEARVAPVAPFPRRLAAPL----- 82  
 QY 52 GSHGFCQGLAEAGPVSYSYSP-----GALVKGKPSRPSOR----- 92  
 DB 83 -G-CG-----RRAAPRPAATHTSPATASGHRRTSCPRGAPSPSPVLTTPAMPQR 135  
 QY 91 CQQR 97  
 DB 136 RNR 140

RESULT 6  
 ID Q8H468 PRELIMINARY; PRT; 1187 AA.  
 AC Q8H468-2003 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
 DE Hypothetical protein.  
 OS Craya sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Eriocaulaceae; Oryzaceae; Oryza.  
 NX NCBI\_TaxID:4550;  
 RN [1] \_SEQUENCE FROM N.A.  
 RP SOURCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Yanamoto K.;  
 RA "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 6, PAC  
 ST Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF001389; BAA32718.1; --  
 DR Genbank; O8405211; HMP.  
 DR PIR; P03578; HMP; 9.  
 DR Pfam; PF03578; HMP; 9.  
 KW Hypothetical protein.  
 KW SEQUENCE 1187 AA; 130328 MW; EECBAAMAAYCC920 CRC64;

Query Match 15.4%; Score 82.5; DB 10; Length 1187;  
 Best Local Similarity 29.5%; Pred. No. 1.5;  
 Matches 36; Conservative 11; Mismatches 34; Indels 41; Gaps 6;  
 QY 3 RRTFAPGAPLGLALLMGHPRAC-----RC-----PPLCV--- 38  
 DB 309 RVVPPAPLANTYWG--GHLFTHRQSPRTGVLTACTSLCRCMASTSPACILL 367  
 QY 39 -AGLAC--GFLG--GWGSHFQSCV--CALFQAVSY--LSPGAPLGR 82  
 DB 368 PVLTACTLGLCRCMASTSPACILGRVPPFPAALYANVTCGLSPFACGR 427  
 QY 83 PF 84  
 DB 428 RB 429

RESULT 7  
 ID Q8H468 PRELIMINARY; PRT; 649 AA.  
 AC Q8H468-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Eriocaulaceae; Oryzaceae; Oryza.  
 NX NCBI\_TaxID:33947.  
 RN [1] \_SEQUENCE FROM N.A.  
 RP SOURCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Yanamoto K.;  
 RA "The Rice Chromosome 10 Sequencing Consortium.  
 ST "In-depth view of structure, activity, and evolution of rice  
 ST chromosome 10.";  
 RT Science 300:1566-1569 (2003).  
 EQ SEQUENCE 649 AA; 71149 MW; EBS212805CDD78 CRC64;

Query Match 15.3%; Score 81.5; DB 10; Length 649;  
 Best Local Similarity 28.8%; Pred. No. 1.1;  
 Matches 30; Conservative 12; Mismatches 33; Indels 29; Gaps 6;  
 QY 2 GRTFAPGAPLGLALLMGHPR--RARGPCLVAGIA--C 44  
 DB 230 GRLRPLRPLVAECLVAGHGSTVPLVYV-----HDTAGLPPLPSSAYTA 281  
 QY 45 GFLG--GWGSHFQSCVQLAEQVSYLSGAPKGRPSQ 87  
 DB 282 GLCRCMASTSPPLACGRVPAHQNIFGDS---RPPPTG 332

RESULT 8  
 ID Q8H468 PRELIMINARY; PRT; 259 AA.  
 AC Q8H468-2003 (TrEMBLrel. 13, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 13, Last sequence update)



[illegible]

Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.  
 ID: Q97QAE; Accession: AK44515.1;  
 KW: Hypothetical protein.  
 SQ: SEQUENCE 598 AA: 58523 MW: 75233 DB1993BDE6 CRC64;

Query Match 14.5% Score 77.5; DB 16; Length 598;  
 Best Local Similarity 28.8%; Pred. No. 2.7;  
 Matches 38; Conservative 7; Mismatches 40; Indels 47; Gaps 7;  
 1 PQRTPRPAP-----SH-----SAPLUG-LALLMHQRPAPCPFLCVAGILAC 44  
 DB 163 PAFSAPVAPVPPLPPNNPAPPSAPVQVPLAPLPSRPAVAVGSLALRIICC 222  
 45 -----GFLGCGSHFQSGC-----QALEPQAVSVLSPPAL----- 79  
 DB 223 RVCVQGLAALNISR-PSCFPPKPAVPAVAGAPVPLPPLPPISTPLPPLPPLP 281  
 80 -----KGRPPSP 86  
 DB 282 ALPTSGAPAPAP 293

## RESULT 15

BLASTN (11) Q97QAE PRELIMINARY: PNT: 992 AA.  
 ID: Q97QAE; Accession: AK44515.1;  
 KW: Hypothetical protein.  
 SQ: SEQUENCE 598 AA: 58523 MW: 75233 DB1993BDE6 CRC64;  
 1 PQRTPRPAP-----SH-----SAPLUG-LALLMHQRPAPCPFLCVAGILAC 44  
 DB 163 PAFSAPVAPVPPLPPNNPAPPSAPVQVPLAPLPSRPAVAVGSLALRIICC 222  
 45 -----GFLGCGSHFQSGC-----QALEPQAVSVLSPPAL----- 79  
 DB 223 RVCVQGLAALNISR-PSCFPPKPAVPAVAGAPVPLPPLPPISTPLPPLPPLP 281  
 80 -----KGRPPSP 86  
 DB 282 ALPTSGAPAPAP 293

Query Match 14.5% Score 77.5; DB 11; Length 992;  
 Best Local Similarity 27.2%; Pred. No. 4.4;  
 Matches 37; Conservative 6; Mismatches 30; Indels 63; Gaps 7;  
 1 PQRTPRPAPSHSAPLUGLALLMHQRPAPCP-----LCVAGILACFLQC 50  
 DB 978 PPAVAVTAPPSPLPVTGA-----PQAPQFQPTQDROSOAGSL----- 920  
 51 WQSHFQSGCL-----QALEPQAVS-----SVLS-----PQAPLKG-- 81  
 DB 921 ----HTDSSCMCTPTPTGLLEPAGPSWPSPLGCGAVLGGKNGKGLPAVLEDAI 976  
 82 ----RPPSPQFQKQOR 94

DB 977 Q97QAEPPAPGAPQOR 992  
 Search completed: March 13, 2004, 07:43:19  
 Job time : 12:59 sec



GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2004, 07:28:59 : Search time 14.1964 Seconds

Title: US-09-836-712-2\_COPY\_1\_97

Sequences: 1: P08787P08787SHPALGCA.....PLKGEPEPEFQDQDQDQDQ 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: Genesecp35Jan04.\*

2: Genesecp35Jan04.\*

3: Genesecp35Jan04.\*

4: Genesecp35Jan04.\*

5: Genesecp35Jan04.\*

6: Genesecp35Jan04.\*

7: Genesecp35Jan04.\*

8: Genesecp35Jan04.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Length	DB ID	Description
1	534	100.0	1416	AB04153	Ab04153 Human ADA
2	492	92.1	1120	AA063829	AA063829 Amino aci
3	492	92.1	1120	AG074113	AG074113 Human mat
4	406	76.0	1427	AD034038	AD034038 Human agg
5	406	76.0	1427	AD034038	AD034038 Human agg
6	204	38.2	242	AA097641	AA097641 Human agg
7	204	38.2	242	AD054011	AD054011 Human agg
8	99.5	18.6	1445	AA098125	AA098125 Human PWW
9	99.5	18.6	1445	AA098125	AA098125 Human PWW
10	93	17.4	115	AA006459	AA006459 Human pol
11	86.5	16.2	398	AB058898	AB058898 Human pol
12	86.5	16.2	398	AB058898	AB058898 Human pol
13	81	15.2	559	AD032956	AD032956 Human nov
14	80.5	15.1	1938	AB076680	AB076680 Streptomy
15	80	15.0	202	AA001892	AA001892 Human pol
16	80	15.0	202	AA001892	AA001892 Human pol
17	79	14.8	117	AA015741	AA015741 Bacterioph
18	79	14.8	412	AB042007	AB042007 Human ova
19	79	14.8	412	AB042007	AB042007 Human ova
20	77	14.6	346	AB043439	AB043439 Human ova
21	77	14.6	346	AB043439	AB043439 Human ova
22	77.5	14.5	598	AB037030	AB037030 Protein e
23	77.5	14.4	461	AA072931	AA072931 Human cul
24	77	14.4	461	AA072931	AA072931 Human cul
25	76.5	14.3	96	AB057403	AB057403 Human pol
26	76.5	14.3	211	AB056617	AB056617 Novel hum

ALIGNMENTS

RESULT 1

AB04153

ID AB04153 standard; protein, 1416 AA.

AC AB04153;

XX 26-MAR-2002 (first entry)

DE Human ADAMS-M polypeptide.

XX Cerebrotic; rheumatoid arthritis; inflammatory bowel disease;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

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XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;

XX Cachexia; allergy; cancer; leukemia; lymphoma; organ transplantation;



DB 15 KAPHSNAPFLGLGLAMQKHPRPCPCVGMVLIACFLGCLGQHPSPQSCQLARQ 74  
 QY 68 ANVSYSISGAPGAPGPPSPFCQQRQR 97  
 DB 75 ANVSYSISGAPGAPGPPSPFCQQRQR 104  
 RESULT 3  
 ID ASG74113 standard; protein; 1120 AA.  
 AC ASG74113;  
 DA 01-MAY-2003 (first entry)  
 DX Human mature zdn5.  
 DE Human; zdn5; ADAM; a disintegrin and metalloprotease; detergent;  
 DX host defence; tumour; extracellular matrix repair; proteolysis;  
 KW apoptosis; angiogenesis; bacterial infection; Crohn's disease;  
 KW degenerative disease; chromosome 9p24; wound healing; TSP-1;  
 KW Thrombospondin domain.  
 CC Homo sapiens.  
 CC  
 CC Key Location/Qualifiers  
 FF Misc-difference 4174a= UNKNOW  
 FF /note= "Encoded by TTN"  
 FT Misc-difference 1118..1119  
 FT /note= "Encoded by CTGGMAT"  
 PN US200212439-A1.  
 CC  
 CC 03-OCT-2002.  
 CC  
 CC 09-FEB-2001; ZC1US-00781080.  
 CC  
 CC 10-FEB-2000; 2000US-016151P.  
 CC (HOLL) HOLLOWAY J L.  
 CC (SHEP) SHEPPARD P O.  
 CC (TAMU) TAMMOTO G O.  
 CC  
 CC Holloway JL, Sheppard PO, Yamamoto G;  
 CC WPI. 2003-174136/17.  
 CC N-PDB; ABX15947, ABX15948.  
 CC  
 CC New zdn5 polypeptides, useful for diagnosing, preventing or treating  
 CC poisoning, melanoma, degenerative disease, bacterial infection, or for  
 CC wound healing.  
 CC  
 CC Claim 2, Page 32-34; 37pp; English.  
 CC  
 CC The invention relates to an isolated polypeptide, zdn5, (a disintegrin  
 CC and metalloprotease (ADAM), the gene for which is located on human  
 CC chromosome 9p24, and a mature polypeptide of the zdn5 protein, zdn5-  
 CC 1 domain (TSP-1) and mature protein. Also included are an isolated  
 CC polynucleotide encoding a fusion protein comprising a first and a second  
 CC polypeptide segments where the first polypeptide segment comprises the  
 CC zdn5 polypeptide and the second polypeptide segment comprises one or  
 CC more (TSP) like domains, and where the first polynucleotide  
 CC segment is positioned amino-terminally to the second polynucleotide  
 CC segment; an expression vector comprising the DNA segment encoding the  
 CC polypeptide comprising the amino acid sequences listed above; and (c) a  
 CC transfection terminator; a cultured cell into which the expression  
 CC vector is transfected; and a method of producing an antibody producing an  
 CC interaction by combining the polypeptides with cells producing an  
 CC antibody to the polypeptide and an isolated immunogenic polypeptide

CC competing at least 10 contiguous amino acids of mature zdn5. The  
 CC polypeptides and polynucleotides are useful for modulating cellular  
 CC interactions. The polypeptides and antibodies to zdn5s are useful for in  
 CC vivo diagnostic or therapeutic applications, such as in identifying or  
 CC characterizing zdn5 gene expression, zdn5 gene expression in a cell,  
 CC complementary molecule. The polypeptides are useful for diagnosing  
 CC preventing or treating tumour formation, Crohn's disease, inflammatory  
 CC bowel disease, food poisoning, melanoma, degenerative disease, bacterial  
 CC infection, Crohn's disease, wound healing, angiogenesis, and host  
 CC healing. The polypeptides are also useful for the study of host defence,  
 CC extracellular matrix repair, proteolysis, apoptosis, angiogenesis and as  
 CC a detergent. The antibodies may be used for tagging cells that express  
 CC zdn5. The polynucleotides are useful for identifying zdn5 gene expression  
 CC assays for determining circulating levels of zdn5 polypeptides. The  
 CC present sequence represents mature zdn5.  
 CC  
 CC Sequence 1120 AA,  
 CC  
 CC Query Match 92.1%; Score 492; DB 6; Length 1120;  
 CC Best Local Similarity 100.0%; Pred. NC 2.9e-42; Indels 0; Gaps 0;  
 CC Matches 90; Conservative 0; Mismatches 0;  
 CC  
 CC QY 8 KAPHSNAPFLGLGLAMQKHPRPCPCVGMVLIACFLGCLGQHPSPQSCQLARQ 67  
 DB 15 KAPHSNAPFLGLGLAMQKHPRPCPCVGMVLIACFLGCLGQHPSPQSCQLARQ 74  
 QY 68 ANVSYSISGAPGAPGPPSPFCQQRQR 97  
 DB 75 ANVSYSISGAPGAPGPPSPFCQQRQR 104  
 RESULT 4  
 ID AAE24450 standard; protein; 1427 AA.  
 CC  
 CC XZ AAE24450;  
 CC XZ AAE24450;  
 CC  
 CC 04-OCT-2002 (first entry)  
 CC  
 CC Human; Von Willebrand factor-cleaving protease (VWF-cp); therapy; enzyme;  
 CC transgenic animal; immunisation; thrombotic disease; preclamping;  
 CC thrombosis; neonatal thrombocytopaenia; haemolytic-uraemic syndrome;  
 CC transgenic; anticoagulant; chromosome 9.  
 CC  
 CC Homo sapiens.  
 CC  
 CC Key Location/Qualifiers  
 FF Peptide 151  
 FF /note= "Signal peptide"  
 FF Protein 52..1427  
 FF /note= "Mature human VWF-cp protein"  
 FF Cleavage-site 69..75  
 FF /note= "Burin cleavage site"  
 FF Region 224..228  
 FF /note= "Catalytic site"  
 FF Region 249  
 FF /note= "Wet turn"  
 FF Domain 301..377  
 FF /note= "Disintegrin like motif"  
 FF Domain /note= "Thrombospondin type I motif"  
 FF Region 441..553  
 FF /note= "Cysteine rich region"  
 FF Region /note= "Spacer"  
 FF Domain 688..743  
 FF /note= "Thrombospondin type I motif"  
 FF Domain /note= "Thrombospondin type I motif"  
 FF Domain 897..952

FT /note: "Thrombospondin type 1 motif"  
 FT 933...1013  
 FT Domain  
 FT 1016...1073  
 FT Domain  
 FT /note: "Thrombospondin type 1 motif"  
 FT 1075...1131  
 FT Domain  
 FT /note: "Thrombospondin type 1 motif"  
 FT 1075...1131  
 FT Domain  
 FT W0200242441-A2.  
 FT XX  
 FT 30-VXV-2002.  
 FT XX  
 FT 22-NOV-2001; 2001NC-EF013391.  
 FT XX  
 FT 22-NOV-2000; 2000US-00721254.  
 FT XX  
 FT 12-APR-2001; 2001US-0083328.  
 FT XX  
 FT (BAXT) BAXTER AG.  
 FT XX  
 FT Laemmle B, Gerritsen HE, Furlan M, Turecek P, Schwarz H;  
 FT Scheiffelinger F, Antoine G, Kerschbaumer R, Zeglavacca L;  
 FT Zimmermann K, Voelkel D;  
 FT N-PEPB; AAD93932.  
 FT WPI; 1479950/51.  
 FT DR N-PEPB; AAD93932.  
 FT DR  
 FT Novel isolated or substantially purified Von Willebrand factor-cleaving  
 FT protease, useful for producing preparation for therapy of thrombosis and  
 FT thromboembolic disease such as thrombotic thrombocytopenic purpura.  
 FT PT  
 FT Claim 1; Fig 5; 9pp; English.  
 FT PD  
 FT The invention relates to an isolated or substantially pure Von Willebrand  
 FT factor (vWF) polypeptide, a vWF polypeptide fragment, a method for  
 FT purifying vWF which involves providing vWF-cp as a ligand, contacting a  
 FT solution comprising vWF with the polypeptide ligand under conditions  
 FT where vWF is bound to the ligand and recovering from the ligand-bound  
 FT vWF solution a purified vWF polypeptide, a vWF polypeptide fragment  
 FT which involves immunizing an animal with vWF-cp and isolating the anti-  
 FT vWF-cp polypeptide antibodies from the animal. vWF-cp is useful for  
 FT producing a preparation of prophylactic or therapeutic thrombotic purpura (TP)  
 FT Henoch-Schönlein purpura, pre-eclampsia, neonatal thrombocytopenia or  
 FT haemolytic-uraemic syndrome. vWF-cp can also be used for processing  
 FT plasmatic or recombinant vWF polypeptides and generating transgenic animals  
 FT which express the polypeptide in vivo. The present sequence is human vWF-cp  
 FT protein. vWF-cp gene is located on chromosome 9  
 FT CC  
 FT Sequence 1427 AA;  
 FT XX  
 FT 50  
 FT Query Match 77.54; Score 414; DB 5; Length 1427;  
 FT Best Local Similarity 0% First 4-14; Indels 0; Gaps 0;  
 FT Mismatches 74; Conservative 0; Mismatches 0;  
 FT QY 24 VHHRRPAPCPVAGIAGLPGILGCGSHFOOCLQALPQAVSVLSPPAKLKP 83  
 FT DB 1 VHHRRPAPCPVAGIAGLPGILGCGSHFOOCLQALPQAVSVLSPPAKLKP 60  
 FT QY 84 PPSPPQPPQPPQPP 97  
 FT DB 61 PPSPPQPPQPPQPP 74  
 FT RESULT 5  
 FT AAD94038 standard; protein; 1427 AA.  
 FT ID AAD94038  
 FT XX AAD94038;  
 FT XX 29-JAN-2004 (first entry)  
 FT DT  
 FT Human aggrecanase protein amino acid sequence.  
 FT DB

XX aggrecanase, aggrecan; articular cartilage, proteoglycan, proteolytic;  
 XX cartilage degradation, osteoarthritis; inflammatory joint disease;  
 XX articular; osteopathic; antiinflammatory;  
 XX aggrecanase-associated disorder; osteoarthritis; inflammatory condition.  
 XX human, enzyme.  
 XX  
 XX Homo sapiens.  
 XX US2003105313-A1.  
 XX 05-JUN-2003.  
 XX 25-JAN-2002; 2002US-00057487.  
 XX 16-OCT-2001; 2001US-00878979.  
 XX (AMSP) AMERICAN HOME PROD CORP.  
 XX  
 XX Racie JA, Twine NC, Agostino MJ, Wolfman N, Morris EA.  
 XX NP; 2003-801251/75.  
 XX N-PEPB; AAD94038.  
 XX  
 XX New isolated DNA molecule encoding an aggrecanase polypeptide for  
 XX producing a purified human aggrecanase protein which can be used to  
 XX develop inhibitors of aggrecanase.  
 XX Claim 14; SEQ ID NO 8; 24pp; English.  
 XX  
 XX This invention relates to a novel human aggrecanase protein and the DNA  
 XX sequence which encodes it. Aggrecan is a major component of the  
 XX cartilage with its mechanical properties of compressability and  
 XX elasticity. A proteolytic activity (aggrecanase) is responsible for the  
 XX cleavage of aggrecan thereby having a deleterious effect on the  
 XX which inhibit the activity of the protein of the invention may have  
 XX articular; osteopathic or antiinflammatory activity. The invention  
 XX may be used to produce a novel human aggrecanase protein and the  
 XX three dimensional structural analysis or computer aided drug design. A  
 XX peptide which binds to aggrecanase is used to inhibit the proteolytic  
 XX degradation of aggrecan. The invention also relates to a method of  
 XX such as, osteoarthritis and other inflammatory conditions. The present  
 XX sequence is that of the human aggrecanase protein (full length sequence)  
 XX of the invention.  
 XX  
 XX Sequence 1427 AA;  
 XX 76.08; Score 405; DB 7; Length 1427;  
 XX Best Local Similarity 38.68; Pred. No. 1.2e-33;  
 XX Matches 73; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX QY 24 VHHRRPAPCPVAGIAGLPGILGCGSHFOOCLQALPQAVSVLSPPAKLKP 83  
 XX DB 1 VHHRRPAPCPVAGIAGLPGILGCGSHFOOCLQALPQAVSVLSPPAKLKP 60  
 XX QY 84 PPSPPQPPQPPQPP 97  
 XX DB 61 PPSPPQPPQPPQPP 74  
 XX RESULT 6  
 XX AAD97641  
 XX ID AAD97641 standard; protein; 242 AA.  
 XX AC AAD97641;  
 XX 27-AUG-2002 (first entry)  
 XX DT  
 XX Human aggrecanase protein.  
 XX DB

XX Aggrasecane, osteoarthritic; antiarthritic; antiinflammatory; human;  
 XX cartilage; osteoarthritis; inflammatory disease; enzyme.  
 XX Homo sapiens.  
 XX CS W0200231093-A2.  
 XX FD 25-APR-2002.  
 XX XX 17-OCT-2001; 2001WC-US0312458.  
 XX PF 17-OCT-2001; 2001US-00057487.  
 XX XX 18-OCT-2000; 2000US-02414699.  
 XX XX (GENY 1 GENETICS INST INC.  
 XX PA Racie LA, Twine NC, Agostino MJ, Wolfman N, Morris EA;  
 XX WPI; 2003-801351/75.  
 XX DR N-PDB; A8K52579.  
 XX DR Novel purified aggrasecane polypeptide useful for developing inhibitors  
 XX and antibodies to the aggrasecane polypeptide, which are useful for  
 XX treating aggrasecane-associated condition such as osteoarthritis.  
 XX Claim 11; Page 33-34; 41pp; English.  
 XX This invention relates to the cDNA and protein sequences of a novel human  
 XX aggrasecane protein, which encodes a major extracellular component of  
 XX articular cartilage. Aggrasecane is a proteoglycan responsible for  
 XX inhibiting the proteolytic activity of aggrecanase, or to inhibit the  
 XX aggrecanase-mediated cleavage of aggrecan in cartilage. The protein of  
 XX the invention is useful for developing inhibitors of aggrasecane protein.  
 XX The invention is also useful for obtaining DNA sequences encoding other  
 XX useful for designing probes for obtaining DNA sequences encoding other  
 XX aggrasecane molecules. The cDNA sequence is also useful for detecting  
 XX mRNA encoding aggrasecane in a given cell population, and thus for  
 XX identifying cells that express aggrasecane. The protein of the invention  
 XX is also useful for preparing vectors for gene therapy applications.  
 XX Aggrasecane is irregularly transcribed or expressed. The DNA sequences  
 XX of the invention are useful for detecting and/or identifying cells with  
 XX characterized by degradation of articular cartilage, by blocking the  
 XX enzyme's proteolytic activity. An aggrasecane protein inhibitor and a  
 XX method for inhibition of its activity are useful for treating various  
 XX conditions associated with degenerative joint disease, such as  
 XX inflammatory disease. The present sequence represents the human  
 XX aggrasecane protein of the invention

XX Sequence 242 AA;  
 XX Query Match: 38.2%; Score 204; DB 7; Length 242;  
 XX E-Value: 1.00E-10; Positives: 36; Gaps: 0;  
 XX Mismatches: 39; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;  
 XX QY 59 SCQLAEFGVAVSYLSFGKALKQRPSPQQRQRQR 97  
 XX AAU7217  
 XX XX 3 SCQLAEFGVAVSYLSFGKALKQRPSPQQRQRQR 41  
 XX DB  
 XX RESULT 8  
 XX ID AAU7217  
 XX XX AAU73217;  
 XX XX Human ADM-7S-like protein.  
 XX DT 15-JUL-2002 (first entry)  
 XX XX Human ADM-7S-like protein.  
 XX XX Human ADM-7S-like protein; cardiovascular disorder; angina;  
 XX vascular system congestive heart failure; myocardial infarction;  
 XX secondary arterial hypertension; peripheral vascular disease; embolism;  
 XX chronic peripheral arterial occlusive disease; acute arterial thrombosis;  
 XX inflammatory vascular disorder; chronic obstructive pulmonary disease;  
 XX liver disease.





XX Homo sapiens.  
 XX NC00006507-A2.  
 XX WC20026507-A2.  
 XX 29-AUG-2002.  
 XX 25-JAN-2002; 2002MO-EP000763.  
 XX 16-FEB-2001; 2001EP-0013779.  
 XX (MERE) MERCK PATENT OMH.  
 XX Hock B, Duester K, Kellner R;  
 XX MPI, 2002-674915/72.  
 XX N-PSDB; AB853396.  
 XX New protein kinase phosphatase interacting partner of 120KD ligand  
 XX polypeptides useful for diagnosing or treating diseases e.g. autism,  
 XX anemia or malignant breast histiocytoma.  
 XX Claim 2; Page 36-38; 41pp; English.  
 XX The present invention relates to a new Protein Kinase Phosphatase  
 XX Interacting Partner of 120KD (PHIP-120) ligand polypeptide. The  
 XX polypeptide is useful for chromosome localisation studies or for  
 XX tissue expression studies. The polypeptide is useful for treating  
 XX diseases. The polypeptide is also useful in diagnostic assays or as  
 XX polynucleotide and polypeptide vaccines. The present amino acid sequence  
 XX represents the human PHIP-120 protein of the invention  
 XX Sequence 1047 AA;  
 XX  
 XX Query Match 16.2%; Score 86.5; DB 5; Length 1047;  
 XX Local Similarity 28%; Conservative 10; Mismatches 38; Indels 37; Gaps 5;  
 XX Matches 28;  
 XX  
 XX 2 GRFTFRKSHSAPLGLALLAMQHQHSPAR-----CPFC-----Y 38  
 XX 258 GPFCQVTHVTP-----PHEPPHPFQALCFACRPEKQSGFALPFLQF 307  
 XX  
 XX 39 AGLACFLGNGSHFQSGCLQA-LEPQNSVYLPQALNKGSPFSPH 89  
 XX 308 GKHGKGTGVALGSLFQQAQAVTFPLGLDAYVSEFLPA--PEPAK 358  
 XX  
 XX RESULT 13  
 XX AUC32856  
 XX ID AUC32856 standard; protein: 539 AA.  
 XX AUC32856;  
 XX 18-DEC-2003 (first entry)  
 XX Human novel contig-encoded polypeptide sequence, SEQ ID NO:3038.  
 XX Human; diagnostic; drug screening; forensics; gene mapping; disease.  
 XX neurodegenerative diseases; anemia; platelet disorder; wound; burns;  
 XX ulcers; osteoporosis; autoimmune disease; cancer;  
 XX molecular weight marker; food supplement; antiparkinsonian; nocrotic;  
 XX antitumor; osteoporosis; immunosuppressive; antiinflammatory; cytostatic;  
 XX gene therapy; chromosome 16.  
 XX Homo sapiens.  
 XX NC0000329271-A2.  
 XX 10-APR-2003.  
 XX

PF 24-SEP-2002; 2002MO-US030474.  
 PR 24-SEP-2001; 2001US-0314631P.  
 XX (HYSE-) HYSEQ INC.  
 XX Tang TT, Zhang J, Ren F, Xue AJ, Zhao QH, Wang J, Wehrman T;  
 XX Zhou P, Ghosh M, Wang D, Ma Y, Aundri V, Wang Z, Weng G;  
 XX Haley-Vicente D, Drenthac RT;  
 XX MPI; 2003-371981/35.  
 XX N-PSDB; AUC32189.  
 XX New polynucleotide and polypeptide useful for diagnosing, preventing or  
 XX treating conditions such as neurodegenerative diseases, anemias, platelet  
 XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 XX cancer.  
 XX Example 2; SEQ ID NO 3038; 1185pp; English.  
 XX The invention relates to 971 novel human cDNA sequences (AUC9919-  
 XX AUC9919) and the polypeptides they encode (AUC90890-AUC91860). The  
 XX invention also relates to nucleic acid sequences over 99% identical with  
 XX the novel human cDNAs. The invention additionally encompasses expression  
 XX vectors, recombinant polynucleotides, recombinant polypeptides, and  
 XX recombinant production of a polypeptide of the invention; an antibody  
 XX against a polypeptide of the invention; a method of detecting  
 XX polynucleotides or polypeptides of the invention; a method of  
 XX expression or activity of polynucleotides or polypeptides of the invention.  
 XX The invention further discloses methods of patenting, treating or  
 XX ameliorating a medical condition; kits comprising polynucleotide probes  
 XX and/or monoclonal antibodies for carrying out the invention; and 767  
 XX contig sequences corresponding to the cDNA sequences of the invention  
 XX (AUC31951, AUC32222) and the polypeptide sequences of the invention  
 XX (AUC31951, AUC32222) and the polypeptide sequences of the invention are  
 XX useful in diagnostics, drug screening, forensics, gene mapping, in the  
 XX identification of mutations responsible for genetic disorders or other  
 XX diseases, for forensic purposes, for the treatment of diseases, or for  
 XX also used for treating diseases such as Parkinson's disease, Alzheimer's  
 XX disease and other neurodegenerative diseases, anemia, platelet  
 XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 XX cancer. The nucleic acid may also be used as hybridisation probes or  
 XX primers, and in the recombinant production of a protein. The polypeptides  
 XX are also useful in generating antibodies, as molecular weight markers,  
 XX in the treatment of diseases, for forensic purposes, for the treatment of  
 XX diseases, or for also used for treating diseases such as Parkinson's  
 XX disease and other neurodegenerative diseases, anemia, platelet  
 XX disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 XX cancer. The polypeptide sequence used in an example of the invention. Note:  
 XX The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic format directly from WFO  
 XX at [http://www.intel.com/pub/indented\\_pat\\_sequences](http://www.intel.com/pub/indented_pat_sequences).  
 XX Sequence 539 AA;  
 XX  
 XX Query Match 15.2%; Score 81; DB 7; Length 539;  
 XX Best Local Similarity 32.5%; Pred. No. 6.1;  
 XX Matches 40; Conservative 7; Mismatches 34; Indels 42; Gaps 9;  
 XX  
 XX 1 RPRTRPRKSHSAPLGLALLAMQHQHSPARCP-L-C----- 37  
 XX 350 GP-FPR-PKX---LQGLASVAPRHPGPPGKPCPCASTLSDPFGFGEAAAE 403  
 XX  
 XX 33 ---VAGTLAGC--FLGNGSHFQSGCLQA--PQNSVYLS--PQALNKGSPFSP 88  
 XX 404 REEVAQGLACPLNLTGMEFVFX-----SCVFGSEDSBQVAMCSFGQPGEPQAPRGR 459  
 XX  
 XX 89 CQK 91  
 XX 460 CQK 462  
 XX  
 XX RESULT 14





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OW protein - protein search, using sw model

Run on: March 11, 2004, 07:43:25 : Search time 7.67917 seconds  
2657.139 Million cell updates/sec

Title: US-09-836-712-2\_COPY\_1\_97

Sequence: 1 PGPSTKPAKSHAPLGLA.....PLKRPSPFQFQRCQRS 97

Scoring table: BLOSUM62

Gapset 31.0, Gapext 0.5

Search: 809742 seqq, 21113259 residues

Total number of hits satisfying chosen parameters: 809742

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\*

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- 2: /cgn2\_6/pdodaca/2/pubpaas/US06\_PUBCOMB.pep.\*
- 3: /cgn2\_6/pdodaca/2/pubpaas/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/pdodaca/2/pubpaas/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/pdodaca/2/pubpaas/US07\_NEW PUB.pep.\*
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- 9: /cgn2\_6/pdodaca/2/pubpaas/US09\_PUBCOMB.pep.\*
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- 14: /cgn2\_6/pdodaca/2/pubpaas/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/pdodaca/2/pubpaas/US10\_PUBCOMB.pep.\*
- 16: /cgn2\_6/pdodaca/2/pubpaas/US10\_NEW PUB.pep.\*
- 17: /cgn2\_6/pdodaca/2/pubpaas/US10\_NEW PUB.pep.\*
- 18: /cgn2\_6/pdodaca/2/pubpaas/US08\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	934	100	0	US-09-836-712-2	Sequence 1, Appl
2	934	100	0	US-09-836-712-2	Sequence 2, Appl
3	414	77.5	62	US-10-222-334-1	Sequence 4, Appl
4	414	77.5	147	US-10-222-334-2	Sequence 2, Appl
5	406	76.2	92	US-09-978-999-8	Sequence 5, Appl
6	366	72.2	94	US-09-978-999-8	Sequence 6, Appl
7	204	38.7	242	US-10-057-487-1	Sequence 1, Appl
8	84	15.2	1760	US-10-369-431-12509	Sequence 1409, A
9	84	15.2	1867	US-10-369-431-12509	Sequence 340, A
10	79	14.8	12	US-10-094-511-340	Sequence 1, Appl
11	79	14.8	412	US-10-264-043-1139	Sequence 3119, A
12	78.5	14.7	146	US-10-264-043-3571	Sequence 3571, A
13	78.5	14.7	146	US-10-264-043-3571	Sequence 3571, A
14	77.6	14.2	22	US-09-837-790-5	Sequence 290, A
15	74.5	14.0	175	US-09-764-877-1158	Sequence 1158, A

Sequence 104, App  
Sequence 104, App  
Sequence 118, Ap  
Sequence 238, Ap  
Sequence 238, Ap  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 3891, Ap  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 128911, A  
Sequence 128911, A  
Sequence 1330, Ap  
Sequence 1330, Ap  
Sequence 110, Ap  
Sequence 110, Ap  
Sequence 1374, Ap  
Sequence 1374, Ap  
Sequence 23, Appl  
Sequence 23, Appl  
Sequence 1454, Ap  
Sequence 1454, Ap  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 3106, Ap  
Sequence 3106, Ap  
Sequence 2061, Ap  
Sequence 2061, Ap  
Sequence 736, Appl  
Sequence 736, Appl  
Sequence 4541, Ap  
Sequence 4, Appl  
Sequence 4, Appl  
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Sequence 4, Appl  
Sequence 156, App  
Sequence 156, App  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 76, Appl  
Sequence 76, Appl

ALIGNMENTS

RESULT 1  
Sequence 2, Application US/09836712  
Patent No. US20010049106A1  
APPLICANT: PFIZER INC.  
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
CURRENT FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO 2: 1  
SEQ ID NO 2: 1  
LENGTH: 1416  
ORGANISM: Human  
US-09-836-712-2

Query Match 100.0% Score 534, DB 9; Length 1416,  
Best Local Similarity 100.0%; Pred. No. 5e+43;  
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 PGPSTKPAKSHAPLGLA.....PLKRPSPFQFQRCQRS 97  
Db 1 PGPSTKPAKSHAPLGLA.....PLKRPSPFQFQRCQRS 97  
Cy 61 LQALEPQAVSLSPFLKGRPPFPQRCQGLR 97  
Db 61 LQALEPQAVSLSPFLKGRPPFPQRCQGLR 97

RESULT 2  
US-05-781-0808-11  
Sequence 1, Application US/097810808  
Sequence 1, Application US/097810808  
GENERAL INFORMATION:  
APPLICANT: HOLLWAY, JIM

```

; APPLICANT: SHEPPARD, PAUL
; APPLICANT: KAWANO, CHIE
; TITLE OF INVENTION: Orogenic Intestinal Peptides.
; FILE REFERENCE: US-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; PRIOR APPLICATION NUMBER: 60/712,334
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1: 1
; LENGTH: 1120
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/SEQ: VARIANT
; LOCATION: (1)...(1120)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-781-0008-11

Query Match 92.1%; Score 492; DB 9; Length 1120;
Best Local Similarity 100.0%; Pred. No. 4,4e-39; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;

QY 8 KAPHSAPLLGLALMGHRRPCPCVAGILACGFLGCGPSPHQSTQLQLEPQ 67
DB 15 KAPHSNAPLLGLALMGHRRPCPCVAGILACGFLGCGPSPHQSTQLQLEPQ 74
QY 66 AVSYSLSPGAPLGPSPSPFQQRQQR 97
DB 75 AVSYSLSPGAPLGPSPSPFQQRQQR 104

RESULT 3
US-10-222-334-4
; Sequence 4, Application US/10222334
; Publication No. US2003007316A1
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Galia
; APPLICANT: Tsai, Han-Mou
; FILE REFERENCE: US-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/01/21,634
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1: 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-334-4

Query Match 77.5%; Score 414; DB 14; Length 842;
Best Local Similarity 100.0%; Pred. No. 1.1e-30;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 83
DB 1 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 60
QY 84 PSFGQPCQRQQR 97
DB 61 PSFGQPCQRQQR 74

RESULT 4
US-10-222-334-2
; Sequence 2, Application US/1022334
; Publication No. US2003007316A1
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Galia
; APPLICANT: Tsai, Han-Mou
; FILE REFERENCE: US-07288
; CURRENT APPLICATION NUMBER: US/10/222,334
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/01/21,634
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1: 1
; LENGTH: 842
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-222-334-2

Query Match 77.5%; Score 414; DB 14; Length 1427;
Best Local Similarity 98.5%; Pred. No. 1.1e-30;
Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 24 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 83
DB 1 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 60
QY 84 PSFGQPCQRQQR 97
DB 61 PSFGQPCQRQQR 74

RESULT 5
US-10-057-487-8
; Sequence 5, Application US/0057487
; Publication No. US2001005191A1
; APPLICANT: Nyeth
; TITLE OF INVENTION: Aggregatase Molecules
; FILE REFERENCE: US-07288
; CURRENT APPLICATION NUMBER: US/10/057,487
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US/01/241,469
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1: 1
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-487-8

Query Match 75.0%; Score 406; DB 14; Length 1427;
Best Local Similarity 98.5%; Pred. No. 1.1e-30;
Matches 73; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 24 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 83
DB 1 MQRHPPACPCPLVAGILACGFLGCGPSPHQSTQLQLEPQAVSYSLSPGAPLGP 60
QY 84 PSFGQPCQRQQR 97
DB 61 PSFGQPCQRQQR 74

RESULT 6
US-98-979-1
; Sequence 1, Application US/0987899
; Patent No. US5002015702A1
; GENERAL INFORMATION:
; APPLICANT: Twine, Lisa A.
; APPLICANT: Twine, Natalie, C.
; APPLICANT: Agostino, Michael, J.
; APPLICANT: Wolfman, Alan, Elizabeth
; APPLICANT: Wolfman, Alan, Elizabeth
; TITLE OF INVENTION: Aggregatase Molecules

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1 PRIOR FILING DATE: 1989-11-03
2 NUMBER OF SEQ ID NOS: 8564
3 SOFTWARE: Patent In Ver. 3.0
4 SEQ NO: 445
5 LENGTH: 415
6 TYPE: PRT
7 ORGANISM: Homo sapiens
8 NAME: KRNK
9 NAME PREV: MISC FEATURE
10 LOCATION: (317)
11 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
12 NAME: MISC FEATURE
13 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
14 US-106-498-4705
15
16 Query Match          14.4% Score 77; DB 14; Length 461;
17 Best Local Similarity 12.7%; Pred No. 20;
18 Matches 32; Conservative 7; Mismatches 43; Indels 16; Gaps
19
20 QY      1 PCGTSPKSHSRDELQALISL-WKHQR-----PRASCPCLVAG--ILACGFLPGC 50
21 DB      36S PATTPSLA-SHTHLGLARVDVEFCMGCFPCPCXPSSEWLSGPMTASC 423
22
23 QY      51 -NDRHFQCQLCNLFQNVNSLSLRAPLKRRSPSQ 87
24 DB      51 -----
25
26 DB      424 GMKSTGGDGLFSVE----SHFWPLVLPTKPKTG 457
27
28 RESULT 14
29 US-09-893-737-290
30 Sequence 230, Application US/09893737
31 BEST LOCAL SIMILARITY 15.4%; Pred No. 11;
32 MATCHES 28; CONSERVATIVE 10; MISMATCHES 10; INDELS 10; GAPS
33 GENERAL INFORMATION
34 APPLICANT: Sheppard, Paul O.
35 TITLE OF INVENTION: MAGMALIAN SECRETED PROTEINS
36 CURRENT FILING DATE: 2001-06-28
37 PRIOR APPLICATION NUMBER: US/09/893,737
38 CURRENT FILING DATE: 2001-06-28
39 PRIOR APPLICATION NUMBER: US 60/215,446
40 NUMBER OF SEQ ID NOS: 328
41 NUMBER OF SEQ ID NOS: 328
42 SOFTWARE: FastSeq for Windows Version 3.0
43 SEQ ID NO 250
44 LENGTH 216
45 TYPE PRT
46 ORGANISM: Homo sapiens
47 US-09-893-737-290
48
49 Query Match          14.2% Score 76; DB 9; Length 216;
50 Best Local Similarity 13.4%; Pred No. 11;
51 Matches 28; Conservative 4; Mismatches 25; Indels 22; Gaps
52
53 QY      15 PLGLGLAHWHQHPHRCPCPLVWGILLACGFLGSGSFQ-CSTGLAEPLGVSVSYLL 73
54 DB      31 PWGLKAGRLGRPP-----PPLCS-----GSHLAGRGLP-RQQVLS-- 69
55
56 QY      74 SQRAELKCRPFPPFQQR 92
57 DB      70 SPQVFEGSLSAFQVHR 88
58
59 RESULT 17
60 US-09-764-877-1158
61 Sequence 1158, Application US/09764877
62 BEST LOCAL SIMILARITY 14.7%; Pred No. 10;
63 MATCHES 28; CONSERVATIVE 14; MISMATCHES 14; INDELS 10; GAPS
64 GENERAL INFORMATION
65 APPLICANT: Rosen et al.
66 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
67 FILE REFERENCE: FC005
68 NUMBER: US/09/764,877
69 CURRENT FILING DATE: 2001-01-17

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: NUMBER OF SEQ ID NOS: 33142
:
: SEQ ID NO 2576
:
: LENGTH: 165
:
: ORGANISM: Pseudomonas aeruginosa
:
: US-09-252-991A-2576
:
:
: Query Match: 15.7% Score 84; DB 4; Length 455;
: Best Local Similarity 28.01; Pred. No. 0.31;
: Matches 33; Conservative 3; Mismatches 37; Indels 40; Gaps 6;
:
: QY 1 PGR-----PTTP--KARSHSAFLGLALLQDQHRPARCFPLCAVGLA 43
:
: DY 46 FPGPARSRRCRCVPTTPTQWTFGAPAFKQVKNVPAIPKAPKSVGVPGLP 105
:
: QY 44 CQFLQWCK-----GESH-----FQSCQLQCEQVMSVSLFQALPKGRPSP 86
:
: DY 106 CG-----WPAKSHPHQHGSGRLGRWQGG-----GEVVCVSESRDAPPPPPPP 155
:
:
: RESULT 3
: US-09-252-991A-27050
: Sequence 30702, Application US/09252991A
: Patent No. 6551795
:
: GENERAL INFORMATION:
: ORGANISM: Pseudomonas aeruginosa
: TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Pseudomonas
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.116 US/08/753.991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR PUBLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
:
: QY 1 SEQ ID NO 7050
:
: DY 1 TYPE: PGR
:
: ORGANISM: Pseudomonas aeruginosa
:
: US-09-252-991A-27050
:
: Query Match: 15.21% Score 81; DB 4; Length 245;
: Best Local Similarity 27.07; Pred. No. 0.32;
: Matches 24; Conservative 11; Mismatches 48; Indels 6; Gaps 2;
:
: QY 6 RPAHSAFLGLALLQDQHRPARCFPLCAVGLACQFLQWGHSPHQSCQALRE 65
:
: DY 68 RPTSGMSVSLFQALPKGRPSPFCQVTKLWAPPS-ASDC-----Q 119
:
: QY 66 FPGMSVSLFQALPKGRPSPFCQVTKLWAPPSFCQVTKLWAPPSFCQVTKL 94
:
: DY 120 FPGMSVSLFQALPKGRPSPFCQVTKLWAPPSFCQVTKLWAPPSFCQVTKL 148
:
:
: RESULT 4
: US-09-252-991A-30702
: Sequence 30702, Application US/09252991A
: Patent No. 6551795
:
: GENERAL INFORMATION:
: ORGANISM: Pseudomonas aeruginosa
: TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Pseudomonas
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.116 US/08/753.991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
:
: QY 1 SEQ ID NO 3142
:
: DY 1 LENGTH: 165

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: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10702

Query Match      15.24; Score 81; DB 4; Length 314;
Best Local       10.33; Fragment 0.02; 35; Indels 34; Gaps 7;
Matches 33; Conservative

QY      11  PPTP-APKASHGATLGLALLR-VQRHPAPCPVCMGLACGLLQCKPESH-PQ 57
QY      14  FORTFPEALQQAQVETPAPVLEPVGSHETALP-----GAGCTHRLD 159
QY      58  GCCLQALQEPQVNSYSPKAPK-----GRPPS-----PPQPR 90
QY      160  RPPHLYQVAPNFDLIA-GTLEPAAEELSFRNKGQVLTLPAAQR 207
DB

RESULT 5
: Sequence 24664, Application US/09252991A
US-09-252-991A-24664
: Patent No 6511795
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF ABSTRACT: NUCLEIC ACID AND AMINO ACID SEQUENCES FOR DIAGNOSTICS AND THERAPEUTICS
: FILING DATE: 107136 136
: CURRENT APPLICATION NUMBER: US/09/252.991A
: PRIORITY CLAIM: YES
: CURRENT FILING DATE: 1999-02-18
: PRIOR FILING DATE NUMBER: 02-18/074, 788
: PRIOR FILING DATE: 1998-09-28
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: PRIORITY CLAIM ID NO: 33142
: SEQ ID NO 24664
: LENGTH: 324
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24664

Query Match Similarity 15.14; Score 80.5; DB 4; Length 324;
Matches 33; Conservative 6; Mismatches 43; Indels 33; Gaps 5;

QY      3  RPTTPASINATLGLALLRMDHP-----RACPPYLVKQSLAC- 45
DB      17  RPTTPSPSPGPR-----KPTPTAGTGVFPRGRRGACR--NMASACAG 63
QY      46  PLOCGHSPQSTCALPQANVSLTPAPKAPRPP-----CPGRCRQR 97
DB      64  FRNSMAPFEDRIVLSALPASSGRPWGGRGPGTTPPPRAGVPTPPEHRK 118

RESULT 6
US-09-252-991A-19528
: Sequence 19528, Application US/09252991A
US-09-252-991A-19528
: Patent No 6511795
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF ABSTRACT: NUCLEIC ACID AND AMINO ACID SEQUENCES FOR DIAGNOSTICS AND THERAPEUTICS
: FILING DATE: 107136 136
: CURRENT APPLICATION NUMBER: US/09252.991A
: PRIORITY CLAIM: YES
: CURRENT FILING DATE NUMBER: 02-18/074, 788
: PRIOR FILING DATE: 1998-09-28
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: PRIORITY CLAIM ID NO: 33142
: SEQ ID NO 19528
: LENGTH: 510
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19528

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Query Match
Best Local Similarity 14.9%; Score 79.5; DB 4; Length 510;
Best Local Similarity 28.2%; Pred. No. 1.1;
Matches 30; Conservative 37; Indels 41; Gaps 7;

OY 2 GPRTPKPSHSAPIGLALLMQR-----QRPFA-----RCPLCTVAGTIL 42
DB 112 GRPGRPFDR-ADVAHPADLQDAVVRHQAQGRVRRRIGACRPAVTCRA 169
DB 43 AGGELGWSHFSQCL--QLPE-----QAVSYLSFGAPLGRPSFGQGR 93
DB 170 -----GPAHRHVVRHQRQFAPQADSAKRYFG--LGRPQCGRLLER 218
OY 94 RQR 97
DB 219 RFR 122

RESULT 7
US-09-836-712-2
Sequence 17616, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136 US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 17616
LENGTH: 510
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17616
Query Match
Best Local Similarity 14.4%; Score 78; DB 4; Length 834;
Matches 30; Conservative 12; Mismatches 28; Indels 62; Gaps 5;

OY 2 GPRTPKPSHSA-----APILGLALLMQR-----HPACPLCTVAGTILG 50
DB 22 GRPGRPFDRSPGRCVAGTILVAVLQPLQPLRHLGHCRCGMA----- 70
OY 51 WFSHFSQCLQALEPQAVSYLSFGP-----APLGRPSF----- 86
DB 71 -----PQASHRAHPAQGRGQEDVAVLVRHRAQLGRSPPLQRLV 115
OY 87 GRPGRQGR 97
DB 116 GRPGRASQ 127

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RESULT 8
US-09-836-712-2
Sequence 21651, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136 US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO: 21651
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21651
Query Match
Best Local Similarity 14.5%; Score 77.5; DB 4; Length 273;
Best Local Similarity 28.4%; Pred. No. 0.87; Indels 46; Gaps 4;
Matches 31; Conservative 8; Mismatches 25;

OY 4 PTPKPSHSA-----PLIGLALLMQRHPA-----RCPLCTVAGTILAC 46
DB 14 PAHPGGRNAGRCGRCGAPRCLCRPPLAPPPAATAATPAAPRPAARAG- 72
OY 47 LLGQWGSHPQSCQLQALEPQAVSYLSFGAPLGRPSFGQGR 96
DB 73 --STRPSPSPSPGTCNVTPDP-----APUSAPAGPEPPDDPSHARR 115

RESULT 9
US-09-252-991A-28706
Sequence 28706, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc; Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136 US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 28706
LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28706
Query Match
Best Local Similarity 14.3%; Score 76; DB 4; Length 445;
Matches 34; Conservative 8; Mismatches 40; Indels 40; Gaps 5;

OY 3 RPTKPSHSAPIGLALLMQR-----PRACPLCTVAGTILAC 44
DB 100 RLRP-AGLRATLGLTFLQAARHLCGQVNPQQLURER-----AA 147
OY 45 GELGQWGSHP-POSCQLQALEPQAVSYLSFGAPLGRPSFGQGR-----QR 94
DB 148 ETVTCQGLSELVFLFLACPAHLSPQGRLELPPACTTMRATATHPQDR 207
OY 95 OR 96
DB 208 HR 209

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RESULT 10
US-09-252-991A-19363
Sequence 19363, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136 US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

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; NUMBER OF SEQ ID NOS: 33142
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US 09-252-991A-17078

Query Match 14,18; Score 75.5; DB 4; Length 330;
Seq. Local Similarity 79.6%; Pred. No. 2.1;
Matches 2; Conservative 17; Mismatches 3;

QY 1 PQRTPKAPSHSAFLGLA-----LLMQHPKAPRCPVLCVAGLACFLGCMQPHF 56
DB 250 PIERPFRSGMGRAGAGRPVLDGRMARCKLCNH-----LPFGAG 238
QY 57 QSCSLALEPQ-----AVSTLSPPAPKRRP 43
DB 299 KQSLAQCPRTGTSKSKAPASLRKP 129

RESULT 11
US-09-252-991A-31668
; Sequence 31668. Application US/09252991A
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25602
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31668

Query Match 14,08; Score 75; DB 4; Length 244;
Seq. Local Similarity 79.6%; Pred. No. 2.9;
Matches 28; Conservative 5; Mismatches 33; Indels 32; Gaps 3;

QY 1 PQRTPKAPSHSAFLGLALH--HQHPKAPRCPVLCVAGLACFLGCMQPHFQ 59
DB 18 PGRSPFRKGRGRTATATLFGHGHQHTQD----- 52
QY 60 CGLAPSPVSTLSPPAPKRRPFPQKQRR 97
DB 53 --QLLOPAVAQSRQDFHG-----PQGRHFRFR 84

RESULT 12
US-09-252-991A-17078
; Sequence 17078. Application US/09252991A
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17078
; LENGTH: 271

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```

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17078

Query Match 13,98; Score 74; DB 4; Length 271;
Seq. Local Similarity 31.3%; Pred. No. 2.1;
Matches 3; Conservative 7; Mismatches 39; Indels 22; Gaps 5;

QY 1 PQRTPKAPSHSAFLGLALH--HQHPKAPRCPVLCVAGLACFLGCMQPHFQ 57
DB 60 PARLRLL--FQHPFRSLRPAQKRRPAPKRRPQKQRR 124
QY 58 QSCSLALEPQAVSTLSPPAPKRRPFPQKQRR 96
DB 135 RPSLQ-----PQGRHFRFR 147

RESULT 13
US-09-252-991A-25602
; Sequence 25602. Application US/09252991A
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25602
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25602

Query Match 13,94; Score 74; DB 4; Length 366;
Seq. Local Similarity 30.6%; Pred. No. 2.9;
Matches 33; Conservative 6; Mismatches 33; Indels 36; Gaps 6;

QY 1 PQRTPKAPSHSAFLGLALH--HQHPKAPRCPVLCVAGLACFLGCMQPHFQ 59
DB 276 PQRTPKAPSHSAFLGLALH--HQHPKAPRCPVLCVAGLACFLGCMQPHFQ 310
QY 60 CGLAPSPVSTLSPPAPKRRPFPQKQRR 97
DB 311 SRSPRPRVAPPRAPKRRPAPKRRPFPQKQRR 358

RESULT 14
US-09-252-991A-29365
; Sequence 29365. Application US/09252991A
; Patent No. 6551795
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29365
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29365

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```
Query Match      13.8%; Score 73.5; DB 4; Length 213;
Best Local Similarity 28.7%; Pred. No. 1.8;
Matches 31; Conservative 9; Mismatches 39; Indels 29; Gaps 6;

OY      1  PGRFTRKAPSHAPL-----LQALLRMRQHPARCFPLCVAGILA--GQFLGCG 52
DB      1  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      21  PVPFGRRFDRPRFPQPAALRRVRSPAPARCFP--AGTLASLCG-----70
DB      21  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      53  PSHQSCQALE-PAQVSYSLSGAPLG--RPSGFGKQGROR 97
DB      53  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      71  -----IFGLAVRRLRAGPQPSGRLRPGQGRVFRQWR 110
DB      71  : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15 991A-39952
US-09-252-991A-39952
Sequence 39952 Application US/09152991A
Patent No. 6551795
GENERAL INFORMATION: Rubeinfeld et al.
TITLE OF INVENTION: NUCLEIC ACIDS AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE 107196.136
CURRENT FILING DATE 1998-03-18
PRIORITY DATE 1998-03-18
PRIORITY APPLICATION NUMBER US 60/074,788
PRIORITY FILING DATE 1998-02-19
PRIORITY APPLICATION NUMBER US 60/094,190
PRIORITY FILING DATE 1998-07-27
NUMBER OF SEQ ID NOS 33142
SEQ ID NO 29952
US-09-252-991A-39952
US-09-252-991A-39952
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-39952

Query Match      13.7%; Score 73; DB 4; Length 286;
Best Local Similarity 32.9%; Pred. No. 2.8;
Matches 27; Conservative 11; Mismatches 28; Indels 16; Gaps 5;

OY      4  PTPKAPS--HSAPLGLALLRMRQHP--PARCFP--LAVAGILAGQFLGCKGSPHQ 57
DB      4  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      212  PRPAPSPANNAP---ALPQSHRPHLLQRTFFPQVCSANVRAHH-----RQAGQ 261
DB      212  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      58  QSCIQALEPQVSYLSLSPAL 79
DB      58  : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      262  RLTLAGSPGQFPSCVATSPV 283
DB      262  : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: March 13, 2004, 07:46:08
Job time : 5.09219 secs
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Oy 179 GAAPRAGLAMPSCRRQLLSLSAGRCWDPF 212  
Db 169 CLTGBSYFSDASWYXKFDQKQILNIP 202

Search completed: March 13, 2004, 07:44:35  
Job time : 6:56771 secB

























- TISSUE SPECIFICITY: Highly expressed in adult and fetal lung, lower expression in brain, placenta, heart, stomach and fetal brain and kidney.

- DOMAIN: The spacer domain and the TSP type-1 domains are important for ligand recognition. The spacer domain has no restrictions on its use by non-protein institutions as long as its content is in no way modified and this statement is not removed, usage by and for commercial entities requires a license agreement (see <http://www.ibs-sib.ch/announcement/>)

- SIMILARITY: Belongs to peptidase family M18.

- FUNCTION: Putative secreted enzyme involved in a stromal endopeptidase (by similarity).

- CATALYTIC ACTIVITY: -

- COFACTOR: -

- SIMILARITY: Contains 2 TSP integrin domain.

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EMBL AF060153; AAC4001.1; .  
GenBank AF060153; AAC7586.1; .  
MIM: 603759; P14583.  
Gene: HNCN124; ADAMTS8.  
MIM: 603759; P14583.  
Gene: HNCN124; ADAMTS8.  
GO: GO:0008439; Fibrinogen binding; TAS  
GO: GO:0007439; Fibrinolytic activity; TAS  
GO: GO:0008483; Fibrinolysis and morphogenesis; TAS  
GO: GO:0008483; Negative regulation of cell proliferation; TAS.  
InterPro: IPR000255; Pept\_M18\_NB.  
InterPro: IPR000255; Pept\_M18\_NB.  
InterPro: IPR001590; Peptidase M18\_N.  
InterPro: IPR004870; Peptidase M18\_N.  
InterPro: IPR000985; TSP\_1.  
Pfam: PF04562; Rep M18 Dropcap 1.  
Pfam: PF04421; Reptovirin; 1.  
PRINTS PR07705; TSP1\_REPEAT.  
SMART: SM00309; TSP1; 2.  
PROSITE: PS00126; ADA\_MPRO1; 1. PALER\_NRG.  
PROSITE: PS0047; DISINTEGRIN; 1. PALER\_NRG.  
PROSITE: PS00593; TSP1; 2.  
PROSITE: PS00593; TSP1; 2.  
PROSITE: PS00144; ZINC\_PROTEASE; 1.  
HMMER HMM000000; Metalloprotease; Zinc signal; Glycoprotein; Zymogen; Hydrolase; Extracellular matrix; Proteolytic cleavage.  
SIGNAL: 1.  
FT PROPEP 1 214 BY SIMILARITY.  
FT CHAIN 1 215 890 ADAMTS-8 PROTEASE.  
FT DOMAIN 1 419 526 DISINTEGRIN-LIKE.  
FT DOMAIN 527 582 TSP TYPE-1 1.  
FT DOMAIN 584 600 CYS-RICH.  
FT DOMAIN 601 617 POLY-P-1.  
FT DOMAIN 618 634 TSP TYPE-1 2.  
FT METAL SITE 364 366 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL SITE 368 368 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 374 374 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 345 345 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 346 346 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 456 456 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 491 491 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 600 600 N-LINKED (GLNAC) (POTENTIAL).  
FT CONFLICT 435 495 YATLGGKGGGELADLPQALPTGH -> FSSGLGKH  
FT CONFLICT 435 440 HHFKVKKGVKKDKKLVKCNF (IN REF. 2).  
SEQUENCE 890 AA: 96671 MR: 57D70RBD3D5739D3 CRC654;  
Query Match 25.0%; Score 285; DB 1; Length 890.  
Local Similarity 39.9%; Pred No. 1e-16;









Repeat: Extracellular matrix.

KW SIGNAL 1 27 POTENTIAL.  
 FT PROPEP 28 1223 BY SIMILARITY.  
 FT METAL 29 1223 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT DOMAIN 224 452 METALLOPROTEASE.  
 FT DOMAIN 453 542 DISINTEGRIN-LIKE.  
 FT DOMAIN 543 568 TSP TYPE-1 1.  
 FT DOMAIN 569 708 CYS-RICH-1.  
 FT DOMAIN 702 779 SPACER.  
 FT DOMAIN 800 860 TSP TYPE-1 2.  
 FT DOMAIN 861 924 TSP TYPE-1 4.  
 FT DOMAIN 925 946 TSP TYPE-1 5.  
 FT DOMAIN 972 1029 TSP TYPE-1 5.  
 FT DOMAIN 1045 1084 PLAC.  
 FT DOMAIN 1085 1100 CYS-RICH-2.  
 FT SITE 200 200 CYSRINS SWITCH (POTENTIAL).  
 FT SITE 201 201 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 389 389 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT ACT SITE 390 390 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT METAL 399 399 ZINC (CATALYTIC) (BY SIMILARITY).  
 FT CARBOHYD 167 167 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 483 483 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 484 484 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 790 790 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 832 832 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 839 839 N-LINKED (GLCNAC - -) (POTENTIAL).  
 FT CARBOHYD 839 839 N-LINKED (GLCNAC - -) (POTENTIAL).  
 SQ SEQUENCE 1095 AA: 89121099 WK: AISC64049475405D CXC64;

Query Match Similarity 24.0% Score 274; DB 1; Length 1095;  
 Conserved 69; Conservative 36; Mismatches 98; Indels 18; Gaps 6;  
 Matches  
 QY 8 LELVAVPVPQAH-QETETVYVNLNIGALLRPSLQGRFVHLVWVYLTTPSCA 66  
 DB 234 VETLVADADVQVHGAEAQHFILVNNVNNFQSLGKIKINQVTLVLRQPAK 293  
 QY 67 ENFANLZSLLSVCKH-----SQTINPEVDFGALVLYITTFLEL-PG 114  
 DB 294 LSIHGHSLESPCHQVEYGGARYLGNVPGSHDPLVDAAVYHTDFCVKDE 353  
 QY 115 KQGVVYVQVQACSEFWGLTPTPQPLQVTHIGHSGLNFGAPSCGQPSVY 174  
 DB 354 PCDTVGIYVGLGVCAKCYCAEENGLNLIATFIHELGNLGNNDL-DHSSCAGRSH 412  
 QY 175 NAGDQAPR--ACLVAPGSGRGLLSLQGRQC--KPP 211  
 DB 413 MSCEWYGRNPSDLNSGSCSEDLNFVSKYVSTLLVTD 453

Search completed: March 13, 2004, 07:39:53  
 Job time : 4.45833 secs



[illegible]

Db	252	VETLVAVTKVYVGVSEVSEVYVLLVMMVTVGLPHSGISGNLVHVVVLLLEBEGQ	311
QY	67	PNVIAVLTSELLVGVGSGVCSINPESDTSCHADVLTATRPDLELDGNN--QVGVTVL	124
Db	312	LAI VHVAKTISLSEVGVGSGVCSINPESDTSCHADVLTATRPDLELDGNN--QVGVTVL	370
QY	132	GVAGVSGTSLCLTETGQVTVGLTVAHIGSLGSLGSLGSGSGSG--HNVASDGA	181
Db	370	GVAGVSGTSLCLTETGQVTVGLTVAHIGSLGSLGSLGSGSGSG--HNVASDGA	429
QY	371	SGMCGVHSCVHMEGSLPLAVLAMELHSGVHGHGHOKE-NCEVPRVPIVMSQIQY	429
Db	182	PRAGLANSPCSRQLSLSLGAGACVWPP	212
QY	430	DPTLVNMSKYSKSTFRLDGRGCFCLDIP	460
Db	252	VETLVAVTKVYVGVSEVSEVYVLLVMMVTVGLPHSGISGNLVHVVVLLLEBEGQ	311
QY	67	PNVIAVLTSELLVGVGSGVCSINPESDTSCHADVLTATRPDLELDGNN--QVGVTVL	124
Db	312	LAI VHVAKTISLSEVGVGSGVCSINPESDTSCHADVLTATRPDLELDGNN--QVGVTVL	370
QY	132	GVAGVSGTSLCLTETGQVTVGLTVAHIGSLGSLGSLGSGSGSG--HNVASDGA	181
Db	370	GVAGVSGTSLCLTETGQVTVGLTVAHIGSLGSLGSLGSGSGSG--HNVASDGA	429
QY	371	SGMCGVHSCVHMEGSLPLAVLAMELHSGVHGHGHOKE-NCEVPRVPIVMSQIQY	429
Db	182	PRAGLANSPCSRQLSLSLGAGACVWPP	212
QY	430	DPTLVNMSKYSKSTFRLDGRGCFCLDIP	460



EA Tupy J.L., Bergman C., Bernan B., Carlson J.M., Calnaker S.E.,  
 EA Clapp M., Drysdale R.L., Smarsh J.B., Price R., De Gray A., Adams N.,  
 EA Serie S.M.J., Smith E.R., Shu S., Smrtniak F., Whiffeld E.,  
 EA Abburner M., Gelbart M.M., Rubin G.M., Muggall C.J., Lewis S.E.,  
 EA Annotations: Drosophila melanogaster  
 EA Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.  
 RU [4]  
 RP SEQUENCE FROM N.A.  
 RP Strains M.D. 28-10001 to the EMBL/GenBank/DBJ databases.  
 RP [5]  
 RP SEQUENCE FROM N.A.  
 RP Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.  
 RU [5]  
 RU EMBL; AF003435; AAF46055.2; --  
 DR HSP, P51567; 1ATU.  
 DR F1yase, F590049793; C04096.  
 DR GO; GO:004222; Zinc ion binding; IEA.  
 DR GO; GO:0008770; Zinc ion binding; IEA.  
 DR GO; GO:0006508; Peptide catabolic activity; IEA.  
 DR InterPro; IPRO1590; Peptide M12B N.  
 DR InterPro; IPRO14870; Peptide M12B N.  
 DR InterPro; IPRO06095; Pept\_M\_En\_Bs.  
 DR InterPro; IPRO08085; TSP.  
 DR Pfam; PF01562; Pept\_M12B\_propep; 1.  
 DR Pfam; PF01421; Reprolysin; 1.  
 DR PRINTS; PR01705; TSP-REPEAT.  
 DR SMART; SM0209; TSP1.2.  
 DR PROSITE; PS0215; ADAM\_MERO; 1.  
 DR PROSITE; PS0142; ZINC\_PROTEASE.  
 DR PROSITE; PS0142; ZINC\_PROTEASE; 1.  
 DR SEQUENCE 1055 AA; 115195 MW; 64369847618P07 C0664;  
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 RU Best Local Similarity 35.0%; Pred. No. 5.6e-22;  
 RU Matches 75; Conservative 31; Mismatches 98; Indels 10; Gaps 5;  
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 RU 7 RUELVANGPVQVQAEVEYVLNLNIGLDELGSLGQFAVLVWVLTPEP; 65  
 DB 331 RUEVLVADATVMSAFRLNGLVYLLNNVSLVXPSLSTGSIIVTVVTLQDESS 389  
 QY 66 APTITANTLSLGVNGSOTINPDTDGHALVLTDFEFLDQNRVOTOL 124  
 DB 390 LQNLVLAQQLQDFQSNQKRGKSGKPHHVALITL--KNTCANNTGLVAY 447  
 QY 125 GRASGFWSLTETDFGLVTHNIGLHGFGLHGDAGSGC---GSGHNSDGA 180  
 DB 448 GSKCKPKXSQVNEHNGHATHTHEGLHFNQFHDHAT--ICHPVPGVPIVHTFG 506  
 QY 181 APRLAGLSPGSRGLLISLAGRCVNDPPT 214  
 DB 507 AUTLVQCSNGSRKVIHTPLDGLGSLDIDPTP 540  
 QY  
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 RU RESULT 6  
 RU Q00028 PRELIMINARY; PRT; 1070 AA.  
 AC Q00028  
 DT 01-MAR-2003 (T-EMBLrel. 23; Created)  
 DT 01-MAR-2003 (T-EMBLrel. 23; Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 25; Last annotation update)  
 DB Mus musculus (Mouse)  
 OS Mus musculus (Mouse)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090  
 RN InterPro; IPRO06095; Pept\_M\_En\_Bs.  
 RN [1]  
 RU SEQUENCE FROM N.A.  
 RU Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.  
 RU [5]  
 RU

RA Bretwaite M., Negaraja E., Abu K.  
 RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 RU [5]  
 RU EMBL; AF528463; AAO17380.1; --  
 DR GO; GO:0004222; Fmetalloendopeptidase activity; IEA.  
 DR GO; GO:0008770; Zinc ion binding; IEA.  
 DR GO; GO:0006508; Peptide catabolic activity; IEA.  
 DR InterPro; IPRO1590; Peptide M12B N.  
 DR InterPro; IPRO16025; Pept\_M\_En\_Bs.  
 DR InterPro; IPRO08085; TSP.  
 DR InterPro; IPRO08085; TSP.  
 DR Pfam; PF01431; Reprolysin; 1.  
 DR Pfam; PF00080; tgp\_1.5.  
 DR PRINTS; PR01705; TSP-REPEAT.  
 DR PROSITE; PS0215; ADAM\_MERO; 1.  
 DR PROSITE; PS0092; TSP1.5.  
 DR PROSITE; PS0142; ZINC\_PROTEASE.  
 DR SEQUENCE 4070 AA; 112125 MW; 689564258A2808 C064;  
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 RU Query Match 27.0%; Score 307.5; D8.11; Length 1070;  
 RU Best Local Similarity 34.8%; Pred. No. 5.4e-19;  
 RU Matches 78; Conservative 34; Mismatches 91; Indels 21; Gaps 7;  
 RU  
 RU 7 RUELVANGPVQVQAEVEYVLNLNIGLDELGSLGQFAVLVWVLTPEP; 65  
 DB 206 RUEVLVADATVMSAFRLNGLVYLLNNVSLVXPSLSTGSIIVTVVTLQDESS 389  
 QY 66 APTITANTLSLGVNGSOTINPDTDGHALVLTDFEFLDQNRVOTOL 124  
 DB 266 TLETHNIGLHGFGLHGDAGSGC---GSGHNSDGA 325  
 QY 115 MRQVQGLQDGSFWSLTETDFGLVTHNIGLHGFGLHGDAGSGC 173  
 DB 336 ---TLLAPVGNQDEERESLNEEDGLGATPTINELHTFDHNDVY--GNCCASGD 381  
 QY 174 ---VWAGDQAFRLAGLSPGSRGLLISLAGRCVNDPPT 213  
 DB 382 PAKLMAHMTKTHPPVWSSSDVITPLDGLGSLNPPR 425  
 RU  
 RU RESULT 7  
 RU Q00026 PRELIMINARY; PRT; 967 AA.  
 ID Q00026  
 AC Q00026 (T-EMBLrel. 22; Created)  
 DT 01-OCT-2002 (T-EMBLrel. 22; Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25; Last annotation update)  
 DB Hypochemical protein.  
 OS Bubo bengalensis (Horseshoe bat)  
 OC Mammalia; Eutharia; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN InterPro; IPRO08085; TSP.  
 RN [1]  
 RU SEQUENCE FROM N.A.  
 RU Submitted (Mar-2003) to the EMBL/GenBank/DBJ databases.  
 RU [5]  
 RU TISSUE-Testis;  
 RA Strauberg R., 2003; to the EMBL/GenBank/DBJ databases.  
 RU EMBL; BC034515; AAN46515.1; --  
 DR GO; GO:0004222; Fmetalloendopeptidase activity; IEA.  
 DR GO; GO:0008770; Zinc ion binding; IEA.  
 DR GO; GO:0006508; Peptide catabolic activity; IEA.  
 DR InterPro; IPRO06586; ADAM\_Cysteine.  
 DR InterPro; IPRO11138; Cycchomere\_F450.  
 DR InterPro; IPRO03870; Peptide M12B N.  
 DR InterPro; IPRO06095; Pept\_M\_En\_Bs.  
 DR InterPro; IPRO08085; TSP.  
 DR Pfam; PF01562; Pept\_M12B\_propep; 1.  
 DR



[illegible]





QY 64 EGAANTANLSSVSGNSINPDDTDPCHADLVITRFL-ELPDQNRGVGT 122  
DB 181 EQL-LINDAAGLNSFGQALVARIKCKKHDA---ILITDQSKWSPGDTLGA 236  
QY 123 QUGAGCSFMSCLITDQGLVIAHIGSLFLEHDAFGSGGCS-CHVASQAA 191  
DB 237 PISQCKSTKCTINEDTGLGIAFIHSGNFWMDV-SNPKAKMNIISPTTG 295  
QY 182 PRAGLANSRCSRLSLGNSRACWQDPR 213  
DB 296 NNQVFNSSCRVKKFLSTQACLVQDVEK 327

## RESULT 15

AC QM156 PRELIMINARY; PRT: 1091 AA.  
AC QM156  
DT 01-MAY-2000 (TRENDEZ. 13, created)  
DT 01-MAY-2000 (TRENDEZ. 13, last sequence update)  
DT 01-MAY-2000 (TRENDEZ. 13, last annotation update)  
QY C31622 protein.  
DB C31622 protein.  
QY C31622 OR BCNA-008694.  
DB C31622 OR BCNA-008694.  
QY CS Drosophila melanogaster (fruit fly).  
DB CS Drosophila melanogaster (fruit fly).  
QY GN Diptera: Insecta: Pterygota;  
DB GN Diptera: Insecta: Pterygota;  
QY OC Neoptera: Diptera: Brachycera; Muscomorpha;  
DB OC Neoptera: Diptera: Brachycera; Muscomorpha;  
QY OC NCBI\_taxid=7227;  
DB OC NCBI\_taxid=7227;  
QY RP SEQUENCE FROM N.A.  
DB RP SEQUENCE FROM N.A.  
QY RX STRAIN=Berkeley;  
DB RX STRAIN=Berkeley;  
QY RX MDLINE=00196006; PubMed=1070112;  
DB RX MDLINE=00196006; PubMed=1070112;  
QY RA Acanthaceae;  
DB RA Acanthaceae;  
QY RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
DB RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
QY RA Sutton G.C., Morcan J.H., C. Zhang Q., Chen J., Pfeiffer B.D.,  
DB RA Sutton G.C., Morcan J.H., C. Zhang Q., Chen J., Pfeiffer B.D.,  
QY RA Wan K.H., Doyle E.G., Hatt G., Nelson C.R., Miklos G.L.G.,  
DB RA Wan K.H., Doyle E.G., Hatt G., Nelson C.R., Miklos G.L.G.,  
QY RA April J.F., Agbayani A., An H.-J., Andrade-Fernandez C., Baldwin D.,  
DB RA April J.F., Agbayani A., An H.-J., Andrade-Fernandez C., Baldwin D.,  
QY RA Balder K.V., Bera P., Bakeman G., Blandini P., Bolshakov S.,  
DB RA Balder K.V., Bera P., Bakeman G., Blandini P., Bolshakov S.,  
QY RA Borkova D., Botchan M.R., Bouck D., Brokstein P., Brottier P.,  
DB RA Borkova D., Botchan M.R., Bouck D., Brokstein P., Brottier P.,  
QY RA Burtis K.C., Busch D.A., Butler H., Cadieu E., Center A., Chandra I.,  
DB RA Burtis K.C., Busch D.A., Butler H., Cadieu E., Center A., Chandra I.,  
QY RA Dabals B., Delcher A., Dong M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
DB RA Dabals B., Delcher A., Dong M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
QY RA Dodson K., Doup L.E., Downes M., Evans C.A., Gocayne J.D.,  
DB RA Dodson K., Doup L.E., Downes M., Evans C.A., Gocayne J.D.,  
QY RA Durbin K.C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
DB RA Durbin K.C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
QY RA Gledits C., Gorrell J., Gu Z., Guan P., Harris M.,  
DB RA Gledits C., Gorrell J., Gu Z., Guan P., Harris M.,  
QY RA Harris R.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
DB RA Harris R.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
QY RA Hostin D., Houston K.A., Howland T.J., Mei W.H., Begwan C.,  
DB RA Hostin D., Houston K.A., Howland T.J., Mei W.H., Begwan C.,  
QY RA Kimmel B., Kodira C., Kraft C., Kravitz S., Kulp D., Lin X.,  
DB RA Kimmel B., Kodira C., Kraft C., Kravitz S., Kulp D., Lin X.,  
QY RA Li X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
DB RA Li X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
QY RA Mount S.M., Xoy M., Murphy B., Murphy L., Murry D.M., Nelson J.L.,  
DB RA Mount S.M., Xoy M., Murphy B., Murphy L., Murry D.M., Nelson J.L.,  
QY RA Nelson D.A., Nelson K.A., Nixon S., Nusker D.R., Pacleb J.M.,  
DB RA Nelson D.A., Nelson K.A., Nixon S., Nusker D.R., Pacleb J.M.,  
QY RA Palazac M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
DB RA Palazac M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
QY RA Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,  
DB RA Shue B.C., Siden-Kiamis I., Simpson M., Skupski M.P., Smith T.,  
QY RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
DB RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
QY RA Swislock R., Tector C., Turner R., Venet S., Wang A.H.,  
DB RA Swislock R., Tector C., Turner R., Venet S., Wang A.H.,  
QY RA Williams S.W., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
DB RA Williams S.W., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
QY Ye J., Yeh R.-F., Zaveri J.S., Zhan X., Zhang G., Zhao X., Zheng L.-G.,  
DB Ye J., Yeh R.-F., Zaveri J.S., Zhan X., Zhang G., Zhao X., Zheng L.-G.,  
QY Zhang X.H., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.-O.,  
DB Zhang X.H., Zhong M., Zhou X., Zhu S., Zhu X., Smith H.-O.,  
QY "The genome sequence of Drosophila melanogaster".  
DB "The genome sequence of Drosophila melanogaster".  
QY RL PMID: 12080800;  
DB RL PMID: 12080800;  
QY RL Science 287:2185-2195(2000).  
DB RL Science 287:2185-2195(2000).  
QY DB  
DB DB

DR CO: 004008270; Fasting ion binding; IEA.  
DR CO: 004006508; P-proteolysis and peptidolysis; IEA.  
DR IncePro: IPR001590; Peptidase M18.  
DR IncePro: IPR006848; Pept\_M18\_DS.  
DR Pfam: PF01431; Reprolysin; 1.  
DR PROSITE: PS00215; ADAM\_MERO; 1.  
DR PROSITE: PS00147; ADAM; 1.  
DR PROSITE: PS00144; 23MC\_PROTASES; 1.  
SQ SEQUENCE 1091 AA; 134074 MW; 5986738F125658E CMC54;  
Query Match  
Best Local Similarity 23.18; Score 263.5; DB: 5; Length 1091;  
Matches 73; Conservative 18; Mismatches 85; Indels 27; Gaps 11;  
QY 6 LHELLLVNVPVQVHQR---DTR---EYVLTVAIGALL-RDPSLQAQFAVHLV 55  
DB 286 LFETAFVNSDL-ANQGVQVTEISKVSEFLAMIR-QVLLVHPTFLARINFLVK 343  
QY 56 KQVIT--RSGCANNTANLSSVSGNSINPDDTDPCHADLVITRFLSLD 113  
DB 344 KLEIKRDPGLVLR-SERVDNTANLSCWKQKLNFSDAQVHAYLVLTGLTLD 402  
QY 114 ---GNEGVGVVQVGLGCSFMSCLITDQGLVIAHIGSLFLEHDAFGSGG 170  
DB 403 KXANSSGVVQVGLGCSFMSCLITDQGLVIAHIGSLFLEHDAFGSGG 461  
QY 171 SGVNASVQDAARFAG---LANSPCSRRSLSLGASRCVQ 210  
DB 462 TWIM----SFLGQGVVNSKCRITLDFMDPQACSLFD 499

Search completed: March 13, 2004, 07:41:15

Job time : 23.1771 secs



CC kinds of secondary arterial hypertension), and peripheral vascular  
 CC diseases (e.g., chronic peripheral arterial occlusive disease, aortic  
 CC aneurysm, atherosclerosis, arteriovenous malformation, etc.).  
 CC liver disorders and chronic obstructive pulmonary disease. The sequences  
 CC are useful in diagnostic assays for detecting diseases and abnormalities  
 CC of nucleic acids and proteins. The sequences are also useful for  
 CC of mutations in the nucleic acid sequences which encode the protein. The  
 CC sequences are also useful for modulating ADAM-TS-like protein activity in  
 CC a disease condition. This sequence represents the human ADAM-TS-like  
 CC protein.

CC Sequence 933 AA;

Query Match: 100.0%, Score 1141, DB 5, Length 933;  
 Best Local Similarity 100.0%; Pred. No. 6, 6e-110;  
 Matches 214; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTATLLELVNVDVFAQDQETVTVTLNGLSLDPSLGAQFVHLVQVVL 60  
 DB 78 AAGCTTATLLELVNVDVFAQDQETVTVTLNGLSLDPSLGAQFVHLVQVVL 60  
 QY 61 TPEPGLNNTANLTSLSLVCNQSQTINPEDTQDGLVLTITFDELPQNVQVG 120  
 DB 138 TPEPGLNNTANLTSLSLVCNQSQTINPEDTQDGLVLTITFDELPQNVQVG 120  
 QY 121 VTQGLGASPTFNSCLITETPDGLVLTITFDELPQNVQVG 180  
 DB 139 VTQGLGASPTFNSCLITETPDGLVLTITFDELPQNVQVG 180  
 QY 181 APFAGLNSPCERQLLSLSAGACVWPDPF 214  
 DB 219 APFAGLNSPCERQLLSLSAGACVWPDPF 214

RESULT 2

AA016618  
 ID AA016618 standard, protein, 1297 AA.

AC AA016618;

XX 15-MAY-2003 (first entry)

DE Human von Willebrand factor (vWF)-cleaving enzyme-related protein #5.

XX Human, von Willebrand factor-cleaving protease, vWF-Cp, therapy; enzyme;  
 XX von Willebrand factor-cleaving protease, vWF-Cp, therapy; enzyme;  
 XX thrombotic thrombocytopenic purpura; TTP; hemolytic-uremic syndrome;  
 XX myocardial infarction; cerebral infarction; arteriosclerosis;  
 XX platelet thrombosis; stenosis.

OS Homo sapiens.

XX WC020286366-A1.

FN 07-NOV-2002.

XX 25-APR-2002; 2002MO-JF004141.

XX 25-APR-2001; 2001JP-02128342.

FR 27-JUL-2001; 2001JP-0227510.

FR 28-SEP-2001; 2001JP-0030297.

XX 25-JUN-2002; 2002JP-00017596.

FA [KAGA] CHENO-SEDO-THERAPUTIC RES INST.

XX Soejima K, Kimura N, Maeda H, Nosaki K, Hamamoto T, Nakagaki T;

XX WPI; 2003-120479/11.

DR N-FDSB; ARF32584.

XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 XX supplementary therapy for thrombotic thrombocytopenic purpura, and for  
 XX developing drugs for e.g. myocardial infarction and cerebral infarction.

CC Claim 4, Page 92-101; 144pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a von  
 CC Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 CC the invention are useful in the diagnosis and treatment of thrombotic  
 CC infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willebrand factor (vWF)-cleaving enzyme-related protein

CC Sequence 1297 AA;

Query Match: 100.0%, Score 1141, DB 6, Length 1297;  
 Best Local Similarity 100.0%; Pred. No. 1, 1e-109;  
 Matches 214; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTATLLELVNVDVFAQDQETVTVTLNGLSLDPSLGAQFVHLVQVVL 60  
 DB 1 AAGCTTATLLELVNVDVFAQDQETVTVTLNGLSLDPSLGAQFVHLVQVVL 60  
 QY 61 TPEPGLNNTANLTSLSLVCNQSQTINPEDTQDGLVLTITFDELPQNVQVG 120  
 DB 61 TPEPGLNNTANLTSLSLVCNQSQTINPEDTQDGLVLTITFDELPQNVQVG 120  
 QY 121 VTQGLGASPTFNSCLITETPDGLVLTITFDELPQNVQVG 180  
 DB 121 VTQGLGASPTFNSCLITETPDGLVLTITFDELPQNVQVG 180  
 QY 181 APFAGLNSPCERQLLSLSAGACVWPDPF 214  
 DB 181 APFAGLNSPCERQLLSLSAGACVWPDPF 214

RESULT 3

AA024449  
 ID AA024449 standard, protein, 1553 AA.

AC AA024449;

XX 04-OCT-2002 (first entry)

DE Human von Willebrand factor-cleaving protease fragment #2.

XX Human, von Willebrand factor-cleaving protease, vWF-Cp, therapy; enzyme;  
 XX von Willebrand factor-cleaving protease, vWF-Cp, therapy; enzyme;  
 XX thrombotic thrombocytopenic purpura; TTP; hemolytic-uremic syndrome;  
 XX myocardial infarction; cerebral infarction; arteriosclerosis;  
 XX platelet thrombosis; stenosis.

OS Homo sapiens.

XX WC020242441-A2.

FN 30-MAY-2002.

XX 25-NOV-2001; 2001WO-EP013391.

FR 22-NOV-2000; 2000US-00721254.

FR 12-APR-2001; 2000US-0083328.

XX (BAXT ) BAXTER AG.

XX Lemmle B, Gerritsen HB, Furlan M, Turecek P, Schwarz H;

XX Schettler F, Gerschmauer K, Raglivaeca L;

XX Schettler F, Voithel D;

XX WPI; 2002-479950/51.

XX Novel isolated or substantially purified von Willebrand factor-cleaving  
 XX protease, useful for producing preparation for therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura.

CC Claim 1, Page 64-68; 93pp; English.

XX The invention relates to an isolated or substantially pure von Willebrand  
 CC factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for  
 CC purifying vWF which involves providing vWF-cp as a ligand, contacting a  
 CC solution comprising vWF with the polypeptide ligand under conditions  
 CC which result in the binding of vWF to the polypeptide ligand, and  
 CC vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies  
 CC which involves immunizing an animal with vWF-cp and isolating the anti-  
 CC vWF cp polypeptide antibodies. The invention also relates to a method of  
 CC treating thrombotic disease and therapy of thrombotic disease.  
 CC Thrombotic disease such as thrombotic thrombocytopenic purpura (TTP),  
 CC Hemolytic-uremic syndrome, disseminated intravascular coagulation, or  
 CC neonatal thrombocytopenia or thrombocytopenia with thrombocytopenia  
 CC plasmatic or recombinantly produced vWF. The invention is useful for  
 CC construction expression systems and generating transgenic animals which  
 CC express the polypeptide in vivo. The present sequence is human vWF-cp  
 CC fragment.

XX Sequence 1353 AA:  
 CC

Query Match 100.0% Score 1141, DB 5, Length 1353,  
 Best Local Similarity 100.0%; Pred. NO. 1.1e-109;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGCILLLELVAVPQVQAGQDTERVYVNLNGLLELDESLGAGQFVLYVQVIL 60  
 DB 1 AAGCILLLELVAVPQVQAGQDTERVYVNLNGLLELDESLGAGQFVLYVQVIL 60  
 QY 61 TPEPGAPNTVNTSSLSVQVSGQNTINPEQDQVYVTRFLELDPQGVQV 120  
 DB 61 TPEPGAPNTVNTSSLSVQVSGQNTINPEQDQVYVTRFLELDPQGVQV 120  
 QY 121 VTQGGACSPFWSCILTEFGDGVTAHSGHLEHFGDNGAGSCGSGHNASQDA 180  
 DB 121 VTQGGACSPFWSCILTEFGDGVTAHSGHLEHFGDNGAGSCGSGHNASQDA 180  
 QY 181 AFRAGLANSFCRQLLSLAGRACVNDPPRP 214  
 DB 181 AFRAGLANSFCRQLLSLAGRACVNDPPRP 214

RESULT 4  
 AAO16617  
 ID AAO16617 standard; protein, 1353 AA.  
 CC

XX AAO16617;  
 CC  
 XX 15-MAY-2003 (first entry)  
 CC  
 XX Human von Willebrand factor (vWF)-cleaving enzyme-related protein #4.  
 DE  
 XX Human, Protease inhibitor; gene therapy; vWF-cleaving enzyme;  
 CC von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 CC

XX Homo sapiens.  
 CC  
 XX M0200289366.XL  
 CC

XX 07-NOV-2002.  
 CC  
 XX 25-APR-2002; 2002NO-JP004141.  
 CC  
 XX 25-APR-2001; 2001JP-00128342.  
 CC  
 XX 27-JUL-2001; 2001JP-00227510.  
 CC  
 XX 28-SEP-2001; 2001JP-00312977.  
 CC  
 XX 23-JUN-2002; 2002JP-00171596.  
 CC

XX [KAGA] CHENKO-BEKO-THERAPEUTIC RES INST.  
 CC  
 XX Seojima K, Mimura N, Nashed H, Nosaki C, Hamamoto T, Nakagaki T;  
 CC

DR WFI\_2003-100479/11.  
 CC

XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 CC for the development of drugs for, e.g., myocardial infarction and cerebral infarction.  
 CC  
 XX Claim 4; Page 92-92; 144pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a von  
 CC Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 CC the invention are useful in the diagnosis and treatment of cerebral  
 CC infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willebrand factor (vWF)-cleaving enzyme-related protein

XX Sequence 1353 AA:  
 CC

Query Match 100.0% Score 1141, DB 6, Length 1353,  
 Best Local Similarity 100.0%; Pred. NO. 1.1e-109;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGCILLLELVAVPQVQAGQDTERVYVNLNGLLELDESLGAGQFVLYVQVIL 60  
 DB 1 AAGCILLLELVAVPQVQAGQDTERVYVNLNGLLELDESLGAGQFVLYVQVIL 60  
 QY 61 TPEPGAPNTVNTSSLSVQVSGQNTINPEQDQVYVTRFLELDPQGVQV 120  
 DB 61 TPEPGAPNTVNTSSLSVQVSGQNTINPEQDQVYVTRFLELDPQGVQV 120  
 QY 121 VTQGGACSPFWSCILTEFGDGVTAHSGHLEHFGDNGAGSCGSGHNASQDA 180  
 DB 121 VTQGGACSPFWSCILTEFGDGVTAHSGHLEHFGDNGAGSCGSGHNASQDA 180  
 QY 181 AFRAGLANSFCRQLLSLAGRACVNDPPRP 214  
 DB 181 AFRAGLANSFCRQLLSLAGRACVNDPPRP 214

RESULT 5  
 ABB04153  
 ID ABB04153 standard; protein, 1416 AA.  
 CC

XX ABB04153;  
 CC  
 XX 26-MAR-2002 (first entry)  
 CC  
 XX Human ADAMTS-M polypeptide.

XX Osteoarthritis; rheumatoid arthritis; inflammatory bowel disease;  
 CC chondrocyte death; osteoporosis; osteoporosis; osteoporosis;  
 KW cachexia; allergy; cancer; leukemia; lymphoma; osteoporosis;  
 CC neurodegenerative disease; congestive heart failure; myocardial infarction; stroke;  
 KW neurodegenerative disease; aneurysm; multiple myeloma;  
 CC infertility; diabetic shock; gene therapy; ADAMTS-M;  
 KW A Disintegrin And Metalloprotease; thrombospondin domain.

XX Homo sapiens.

XX Key Location/Qualifiers  
 CC Peptide  
 CC /label= Prodomain  
 CC /note= "The mature form of the ADAMTS-M protein is  
 CC processed by furin cleavage of the prodomain"  
 CC  
 CC Cleavage-site  
 CC /label= Furin\_cleavage\_site  
 CC Protein 98..1416  
 CC /label= Mature ADAMTS-M protein  
 CC /note= "The mature form of the ADAMTS-M protein is  
 CC processed by furin cleavage of the prodomain"  
 CC 98..311  
 CC Domain

FT Domain /label= Metalloprotease\_domain  
FT 2476-272 /label= Zinc-binding motif  
FT 324-334 Domain  
FT 410-473 /label= Disintegrin\_domain  
FT 410-473 Domain  
FT 410-473 /label= Thrombospondin\_submotif  
FT 419-424 Domain  
FT 419-424 /label= Thrombospondin-binding\_domain  
FT 1099-1156 Domain  
FT 1099-1156 /label= Thrombospondin\_submotif  
XX EP151055-A1.  
XX NOV-2001.  
XX 07-NOV-2001.  
XX 24-APR-2001; 2001EP-00103706.  
XX 27-APR-2000; 2000US-02000409.  
XX (PFTZ ) PFIZER PHRO INC.  
XX Buckinder L, Mitchell PG, Wachtmann TS, Walsh RT;  
XX MPI. 2002-084275/12.  
XX N-PDS; ASA02549.  
XX New polynucleotide, useful in gene therapy, particularly for treating or  
XX rheumatoid arthritis, Crohn's disease, Alzheimer's disease and organ  
XX transplant toxicity and rejection, comprises ADAMTS polynucleotide and an  
XX encoded polypeptide.  
XX Claim 4; Fig 2; 3pp; English.  
XX The present sequence represents a ADAMTS protein designated ADAMTS-M,  
XX Metalloprotease family of metalloproteases, and contains a  
XX thrombospondin domain (TS). The protein is encoded by the cDNA given in  
XX ADAM2549. The specification describes a newly isolated polynucleotide,  
XX given in the specification, or a metalloprotease, disintegrin domain,  
XX predominant or its thrombospondin submotif. The polynucleotide, polypeptide  
XX and agent are useful for manufacturing a medicament for treating  
XX polynucleotide ADAMTS-M polypeptide and agent are useful for  
XX manufacturing a medicament for treating arthritis (osteoarthritis and  
XX rheumatoid arthritis), inflammatory bowel disease, Crohn's disease,  
XX osteoporosis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis,  
XX cachexia, allergy, cancer (e.g. solid tumour cancer including colon,  
XX breast, lung, prostate, brain or haematopoietic malignancies including  
XX leukaemia and lymphoma), osteoporosis, osteoarthritis, osteoarthritis,  
XX spinal cord injury, neurodegenerative disease, autoimmune disorders,  
XX Huntington's disease, Parkinson's disease, migraine, pain, depression,  
XX multiple sclerosis, schizophrenia and post-traumatic stress disorder.  
XX The polynucleotide and polypeptide are also useful for  
XX diagnosing the diseases above. The polynucleotide is particularly useful  
XX in gene therapy for treating the diseases cited above  
XX Sequence 1416 AA;  
XX  
XX Query Match 100.0%; Score 1141; DB 5; Length 1416;  
XX Match 100.0%; Similarity 100.0%; Positives 26; Negatives 0;  
XX Mchz 214; Conservative 0; Mismatches 0;  
QY 1 AAGGILELLVANGPVQAGQEDERYVLTNLGALLDLSGAGFVAVWVIL 60  
PR 98 AAGGILELLVANGPVQAGQEDERYVLTNLGALLDLSGAGFVAVWVIL 157  
Db 61 TSPCAPNTALLISLVGSGQTINPEDTDFRADLVITTFELFPGKRWG 120  
Db 158 TSPCAPNTALLISLVGSGQTINPEDTDFRADLVITTFELFPGKRWG 217

QY 121 VTDLGAGSPFSLTSTEDTQFLVNTIETGSHQHGARGSGGSHWASDGA 160  
Db 218 VTDLGAGSPFSLTSTEDTQFLVNTIETGSHQHGARGSGGSHWASDGA 277  
QY 181 APPAGLANSCRSQSLLSGAGRCACWDPDP 214  
Db 278 APPAGLANSCRSQSLLSGAGRCACWDPDP 311  
RESULT 6  
AA022450  
XX AA0224450 standard; protein; 1427 AA.  
XX AA0224450/  
XX AC AA0224450/  
XX 04-OCT-2002 (first entry)  
XX Human Von Willebrand factor-cleaving protease (VWF-cp) .  
XX Human; Von Willebrand factor-cleaving protease; VWF-cp; therapy; enzyme;  
XX transgenic animal; immunisation; thrombotic disease; preclampsia;  
XX thrombotic thrombocytopenic purpura; TTP; Henoch-Schönlein purpura;  
XX thrombosis; neonatal thrombocytopenia; haemolytic-uraemic syndrome;  
XX transgenic; antithrombin; thrombosis.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX 1..51 /label= Signal\_Peptide  
XX 69..75 /label= Mature human VWF-cp protein  
XX 69..75 /label= Purin cleavage site  
XX 249 /label= Catalytic site  
XX 249 /label= Catalytic site  
XX 387..439 /label= Distintegrin like motif  
XX 387..439 /label= Thrombospondin type I motif  
XX 554..687 /label= Cysteine rich region  
XX 554..687 /label= Spacer  
XX 744..805 /label= Thrombospondin type I motif  
XX 905..955 /label= Thrombospondin type I motif  
XX 953..1013 /label= Thrombospondin type I motif  
XX 1005..1075 /label= Thrombospondin type I motif  
XX 1075..1131 /label= Thrombospondin type I motif  
XX 1075..1131 /label= Thrombospondin type I motif  
XX W0200224451-A2.  
XX 30-NOV-2002.  
XX 30-NOV-2001; 2001MO-EP013391.  
XX 29-NOV-2000; 2000US-00721254.  
XX 12-APR-2001; 2001US-00433328.  
XX (BAXT ) BAXTER AG.  
XX Laemmle B, Gerritsen HE, Eurlen M, Turecek P, Schwarz H;  
XX Schallinger F, Antoine G, Kerschbaumer R, Tagliavacca L;  
XX Zimmermann K, Voelkel D;

XX NPI: 2002-479950/51.  
 XX N-PSDB; AA039332.  
 XX Novel isolated or substantially purified von Willebrand factor-cleaving  
 XX protease, useful for producing preparation for therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura.  
 XX Claim 1; Fig 5; 93pp; English.  
 XX The invention relates to an isolated or substantially pure von Willebrand  
 XX factor (vWF) polypeptide, a purified vWF polypeptide, a purified vWF  
 XX polypeptide which involves providing vWF-cp as a ligand, contacting a  
 XX solution comprising vWF with the polypeptide ligand under conditions  
 XX where vWF is bound to the ligand and recovering from the ligand purified  
 XX vWF, and a method for producing a purified vWF polypeptide, which  
 XX involves immunising an animal with vWF-cp and isolating the anti-  
 XX vWF cp polypeptide antibodies from the animal. vWF-cp is useful for  
 XX producing a preparation of prophylaxis and therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura or  
 XX Henoch-Schönlein purpura, pre-eclampsia, neonatal thrombocytopenia or  
 XX haemolytic-uraemic syndrome. vWF-cp can also be used for processing  
 XX plasmatic or recombinantly produced vWF. The invention is useful for  
 XX expressing the polypeptide in vivo. The present sequence is human vWF-cp  
 XX protein. vWF-cp gene is located on chromosome 9  
 XX Sequence 1427 AA;  
 XX Query Match 100.0%; Score 1141; DB 5; Length 1427;  
 XX Best Local Similarity 100.0%; First NCBI 146-105; Gaps 0;  
 XX Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAGGDIHLLVAVDPVQAGQDTERVLTNINIGALLKPSLSGAFVHVLVWVIL 60  
 DB 75 AAGGDIHLLVAVDPVQAGQDTERVLTNINIGALLKPSLSGAFVHVLVWVIL 134  
 OY 61 TEPFGAPNITANTLSLVCNGQNTINPEDTTPGADLVLTITFLELPQNRQNG 120  
 DB 135 TEPFGAPNITANTLSLVCNGQNTINPEDTTPGADLVLTITFLELPQNRQNG 194  
 OY 121 VTQAGKSPFWCLTETDTPGDLVLTINELISFLELDNAPGSCGPGHVAQVRA 180  
 DB 195 VTQAGKSPFWCLTETDTPGDLVLTINELISFLELDNAPGSCGPGHVAQVRA 254  
 OY 181 AFRAGLWSPCSRQLLSLISAGRCVWPPRP 214  
 DB 255 AFRAGLWSPCSRQLLSLISAGRCVWPPRP 288  
 XX RESULT 7  
 XX ID ADD94038 standard; protein; 1427 AA.  
 XX XX ADD94038;  
 XX XX 29-JAN-2004 (first entry)  
 XX XX Human aggrecanase protein amino acid sequence.  
 XX XX aggrecanase; aggrecan; articular cartilage; proteoglycan; proteolytic;  
 XX XX cartilage degradation; osteoarthritis; inflammatory joint disease;  
 XX XX aggrecanase-associated disorder; osteoarthritis; inflammatory condition;  
 XX XX human; enzyme.  
 XX XX Homo sapiens.  
 XX XX US200310513-A1.  
 XX XX 05-JUN-2003.  
 XX XX 25-JAN-2002; 2002US-00057487.

XX NPI: 2002-479950/51.  
 XX N-PSDB; AA039332.  
 XX Novel isolated or substantially purified von Willebrand factor-cleaving  
 XX protease, useful for producing preparation for therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura.  
 XX Claim 1; Fig 5; 93pp; English.  
 XX The invention relates to an isolated or substantially pure von Willebrand  
 XX factor (vWF) polypeptide, a purified vWF polypeptide, a purified vWF  
 XX polypeptide which involves providing vWF-cp as a ligand, contacting a  
 XX solution comprising vWF with the polypeptide ligand under conditions  
 XX where vWF is bound to the ligand and recovering from the ligand purified  
 XX vWF, and a method for producing a purified vWF polypeptide, which  
 XX involves immunising an animal with vWF-cp and isolating the anti-  
 XX vWF cp polypeptide antibodies from the animal. vWF-cp is useful for  
 XX producing a preparation of prophylaxis and therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura or  
 XX Henoch-Schönlein purpura, pre-eclampsia, neonatal thrombocytopenia or  
 XX haemolytic-uraemic syndrome. vWF-cp can also be used for processing  
 XX plasmatic or recombinantly produced vWF. The invention is useful for  
 XX expressing the polypeptide in vivo. The present sequence is human vWF-cp  
 XX protein. vWF-cp gene is located on chromosome 9  
 XX Sequence 1427 AA;  
 XX Query Match 100.0%; Score 1141; DB 7; Length 1427;  
 XX Best Local Similarity 100.0%; First NCBI 146-105; Gaps 0;  
 XX Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAGGDIHLLVAVDPVQAGQDTERVLTNINIGALLKPSLSGAFVHVLVWVIL 60  
 DB 75 AAGGDIHLLVAVDPVQAGQDTERVLTNINIGALLKPSLSGAFVHVLVWVIL 134  
 OY 61 TEPFGAPNITANTLSLVCNGQNTINPEDTTPGADLVLTITFLELPQNRQNG 120  
 DB 135 TEPFGAPNITANTLSLVCNGQNTINPEDTTPGADLVLTITFLELPQNRQNG 194  
 OY 121 VTQAGKSPFWCLTETDTPGDLVLTINELISFLELDNAPGSCGPGHVAQVRA 180  
 DB 195 VTQAGKSPFWCLTETDTPGDLVLTINELISFLELDNAPGSCGPGHVAQVRA 254  
 OY 181 AFRAGLWSPCSRQLLSLISAGRCVWPPRP 214  
 DB 255 AFRAGLWSPCSRQLLSLISAGRCVWPPRP 288  
 XX RESULT 8  
 XX ID AB898125 standard; protein; 1445 AA.  
 XX XX AB898125;  
 XX XX 17-OCT-2002 (first entry)  
 XX XX Human P90W Injeye ID 7473607CBL.  
 XX XX Human; P90W; protein modification and maintenance molecule;  
 XX XX anti-infective; chemotherapeutic; antidiabetic; antiparkinsonian;  
 XX XX antineoplastic; dermatological; antitubercular; antiparkinsonian;  
 XX XX antianemic; anti-inflammatory; antitumor; antineoplastic; antineoplastic;  
 XX XX hepatotropic; osteopathic; antiemetic; antipyretic; virucide;



Db 121 VTOLGACSPFMSCLITETGFDLGVTHAEIGHSGFLEHDAQSGQSGHVMASDGA 180

Oy 181 AFAAGLAMPSCSRQLLSLSAGAR 206

Db 181 AFAAGLAMPSCSRQLLSLSAGAR 206

Db 181 AFAAGLAMPSCSRQLLSLSAGAR 206

RESULT 13

Id AAO16620 standard; protein; 1323 AA.

Xx AAO16620;

Xx AAO16620;

Dt 15-MAY-2003 (first entry)

Xx Human von Willebrand factor (vWF)-cleaving enzyme-related protein W7.

Xx Human; protease inhibitor; gene therapy; vWF-cleaving enzyme;

Xx von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;

Xx myocardial infarction; cerebral infarction; arteriosclerosis;

Xx platelet thrombosis; stenosis.

Xx Homo sapiens.

Xx NC0200288366-A1.

Pn NC0200288366-A1.

Xx 07-NOV-2002.

Dt 25-APR-2002; 2002MO-JF004141.

Pf 25-APR-2001; 2001JP-00138143.

Xx 25-APR-2001; 2001JP-00227610.

Pr 27-JUL-2001; 2001JP-00227610.

Pr 28-SEP-2001; 2001JP-00303977.

Pr 28-SEP-2001; 2001JP-00303977.

Pr 25-JAN-2002; 2002JP-00017596.

Pr 25-JAN-2002; 2002JP-00017596.

Pa (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Pi Soejima K, Mimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;

Pt WPI; 2003-120479/11.

Dr N-PDS; ART32586.

CC von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and supplementary therapy for, thrombotic thrombocytopenic purpura, and for developing drugs for e.g. myocardial infarction and cerebral infarction.

CC Claim 4; Page 112-121; 144pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a von Willebrand factor (vWF)-cleaving enzyme. The invention also comprises sequences of the invention useful in the diagnosis and treatment of thrombotic thrombocytopenic purpura, and in developing drugs for myocardial infarction, cerebral infarction, arteriosclerosis, platelet thrombosis, and stenosis. The present amino acid sequence represents a human von Willebrand factor (vWF)-cleaving enzyme-related protein.

CC Sequence 1323 AA:

Query Watch 93.3%; Score 1065; Ds 6; Length 1323;

Best Local Similarity 98.1%; Pred. No. 1e-101;

Matches 202; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AGGILHLHLVAVGPPQAFQEDTERTYVLTNMGALLRDFSLGQAFVLLVWVIL 60

Db 1 AGGILHLHLVAVGPPQAFQEDTERTYVLTNMGALLRDFSLGQAFVLLVWVIL 60

Oy 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Db 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Oy 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Db 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Oy 121 VTOLGACSPFMSCLITETGFDLGVTHAEIGHSGFLEHDAQSGQSGHVMASDGA 180

Db 121 VTOLGACSPFMSCLITETGFDLGVTHAEIGHSGFLEHDAQSGQSGHVMASDGA 180

Oy 181 AFAAGLAMPSCSRQLLSLSAGAR 206

Db 181 AFAAGLAMPSCSRQLLSLSAGAR 206

Db 181 AFAAGLAMPSCSRQLLSLSAGAR 206

RESULT 11

Id AAO16619 standard; protein; 1378 AA.

Xx AAO16619;

Xx AAO16619;

Dt 15-MAY-2003 (first entry)

Xx Human von Willebrand factor (vWF)-cleaving enzyme-related protein #6.

Xx Human; protease inhibitor; gene therapy; vWF-cleaving enzyme;

Xx von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;

Xx myocardial infarction; cerebral infarction; arteriosclerosis;

Xx platelet thrombosis; stenosis.

Xx Homo sapiens.

Xx NC0200288366-A1.

Pn NC0200288366-A1.

Xx 07-NOV-2002.

Dt 25-APR-2002; 2002MO-JF004141.

Pf 25-APR-2001; 2001JP-00138142.

Xx 25-APR-2001; 2001JP-00227612.

Pr 27-JUL-2001; 2001JP-00227612.

Pr 28-SEP-2001; 2001JP-00303977.

Pr 28-SEP-2001; 2001JP-00303977.

Pr 25-JAN-2002; 2002JP-00017596.

Pr 25-JAN-2002; 2002JP-00017596.

Pa (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.

Pi Soejima K, Mimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;

Pt WPI; 2003-120479/11.

Dr N-PDS; ART32586.

CC von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and supplementary therapy for, thrombotic thrombocytopenic purpura, and for developing drugs for e.g. myocardial infarction and cerebral infarction.

CC Claim 4; Page 102-111; 144pp; Japanese.

CC The invention comprises the amino acid and coding sequence of a von Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of the invention also comprise sequences of the invention useful in the diagnosis of thrombocytopenic purpura, and in developing drugs for myocardial infarction, cerebral infarction, arteriosclerosis, platelet thrombosis, and stenosis. The present amino acid sequence represents a human von Willebrand factor (vWF)-cleaving enzyme-related protein.

CC Sequence 1378 AA:

Query Watch 93.3%; Score 1065; Ds 6; Length 1378;

Best Local Similarity 98.1%; Pred. No. 1e-101;

Matches 202; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 AGGILHLHLVAVGPPQAFQEDTERTYVLTNMGALLRDFSLGQAFVLLVWVIL 60

Db 1 AGGILHLHLVAVGPPQAFQEDTERTYVLTNMGALLRDFSLGQAFVLLVWVIL 60

Oy 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Db 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Oy 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Db 61 TEPGKAPNTANLTSLSVCGSQNTINFDPTDQADVLVITFDLEFDGNQVRG 120

Oy 121 VTOLGACSPFMSCLITETGFDLGVTHAEIGHSGFLEHDAQSGQSGHVMASDGA 180

Db 121 VTOLGACSPFMSCLITETGFDLGVTHAEIGHSGFLEHDAQSGQSGHVMASDGA 180



Qy 181. AFRAGLANSFCPSRQRLSLLSLGGSHAR 206  
Db 181. AFRAGLANSFCPSRQRLSLLSLGGSHAR 206

RESULT 12  
ID AAO16622 standard; protein, 270 AA.  
XX AA  
XX AA  
XX AAO16622;  
XX AA  
XX 15-MAY-2003 (first entry)  
XX AA  
XX Human von Willebrand factor  
XX AA  
XX Human, protease inhibitor, gene therapy, vWF-cleaving enzyme,  
XX AA  
XX myocardial infarction; cerebral infarction; arteriosclerosis;  
XX AA  
XX platelet thrombosis; stenosis.  
XX AA  
XX Homo sapiens.  
XX AA  
XX WC020286366-A1.  
XX FN  
XX 07-NOV-2002.  
XX AA  
XX 25-APR-2002; 2002MO-JP0041-41.  
XX PF  
XX 25-APR-2001; 2001JP-00128342.  
XX PR  
XX 27-JUL-2001; 2001JP-00227510.  
XX PR  
XX 28-SEP-2001; 2001JP-00302877.  
XX PR  
XX 25-JAN-2002; 2002JP-00017596.  
XX AA  
XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
XX AA  
XX Soejima K, Misura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;  
XX WPI; 2003-120479/11.  
XX DR  
XX N-PSDB; AFR32588.  
XX AA  
XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
XX AA  
XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
XX AA  
XX developing drugs for e.g. myocardial infarction and cerebral infarction.  
XX AA  
XX Claim 4, Page 124-126; 14pp; Japanese.  
XX AA  
XX The invention comprises the amino acid and coding sequence of a von  
XX AA  
XX Willebrand factor-cleaving enzyme, and the amino acid and coding sequences of  
XX AA  
XX the invention are useful in the diagnosis and treatment of  
XX AA  
XX thrombocytopenic purpura, and in developing drugs for myocardial  
XX AA  
XX infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
XX AA  
XX stenosis, and stenosis, and as a human von  
XX AA  
XX Willebrand factor (vWF)-cleaving enzyme-related protein  
XX AA  
XX Sequence 270 AA;  
XX AA  
XX Query Match 32.94; Score 1051.5; DB 6; Length 270;  
XX AA  
XX Best Local Similarity 95.84; Pred. No. 3.8e-102;  
XX AA  
XX Matches 205; Conservative 0; X mismatches 2; Indels 7; Gaps 2;  
XX AA

Qy 1 AAGGHLLELVANGVPDQVQNGESTERYVTNLGALLHDPSSLGAGFVHLVXVWIL 60  
Db 1 AAGGHLLELVANGVPDQVQNGESTERYVTNLGALLHDPSSLGAGFVHLVXVWIL 60  
Qy 61 TEPGAPNTANLTSLSVGGSGTINPDPDQALVLYTFHLELPQGNVRG 120  
Db 61 TEPGAPNTANLTSLSVGGSGTINPDPDQALVLYTFHLELPQGNVRG 120  
Qy 121 VTQLGAGSPFNLCTETQDFGLVGTAEHIGFSLHGGVGGSGQSGHAWDRA 180  
Db 121 VTQLGAGSPFNLCTETQDFGLVGTAEHIGFSLHGGVGGSGQSGHAWDRA 180  
Qy 181 AFRAGLANSFCPSRQRLSLLSLGGSHAR 206  
Db 181 AFRAGLANSFCPSRQRLSLLSLGGSHAR 206

Qy 181. AFRAGLANSFCPSRQRLSLLSLGGSHAR 206  
Db 181. AFRAGLANSFCPSRQRLSLLSLGGSHAR 206

RESULT 13  
ID AAU97641 standard; protein, 242 AA.  
XX AA  
XX AAU97641;  
XX AA  
XX 27-AUG-2002 (first entry)  
XX AA  
XX Human aggrecanase protein.  
XX AA  
XX Aggrecanase; osteopontin; antiarthritic; antiinflammatory; human;  
XX AA  
XX cartilage; osteoarthritis; inflammatory disease; enzyme.  
XX AA  
XX Homo sapiens.  
XX AA  
XX WC020233093-A2.  
XX FN  
XX 25-APR-2002.  
XX AA  
XX 17-OCT-2001; 2001WO-US032458.  
XX PR  
XX 18-OCT-2000; 2000US-0241463P.  
XX AA  
XX (GENY) GENETICS INST INC.  
XX AA  
XX Racie LA, Twine NC, Agostino NJ, Wolfman NM, Morris BA;  
XX PT  
XX WPI; 2003-45403/48.  
XX DR  
XX N-PSDB; AHS24573.  
XX AA  
XX Novel purified aggrecanase polypeptide useful for developing inhibitors  
XX AA  
XX thereof, and a polypeptide which is useful for  
XX AA  
XX treating aggrecanase-associated condition such as osteoarthritis  
XX AA  
XX Claim 11; Page 33-34; 41pp; English.  
XX AA  
XX This invention relates to the cDNA and protein sequences of a novel human  
XX AA  
XX aggrecanase polypeptide. The protein of the invention may be used to  
XX AA  
XX inhibit the proteolytic activity of aggrecan in cartilage. The protein of  
XX AA  
XX the invention is useful for developing inhibitors of aggrecanase protein.  
XX AA  
XX The cDNA sequence encoding the aggrecanase protein of the invention is  
XX AA  
XX useful for designing probes for detecting aggrecanase mRNA, and thus for  
XX AA  
XX detecting aggrecanase mRNA in a given cell population, and thus for  
XX AA  
XX detecting or diagnosing genetic disorders involving the aggrecanase, or  
XX AA  
XX disorders involving aggrecanase protein. The cDNA sequence encoding the  
XX AA  
XX aggrecanase is preferably transcribed or expressed. The DNA sequences  
XX AA  
XX may also be useful for preparing vectors for gene therapy applications.  
XX AA  
XX An inhibitor of the protein is useful in treating conditions making the  
XX AA  
XX character of aggrecanase protein activity. An aggrecanase protein inhibitor and a  
XX AA  
XX method for inhibition of its activity are useful for treating various  
XX AA  
XX aggrecanase-associated conditions including osteoarthritis and other  
XX AA  
XX inflammatory diseases. The present invention also provides a sequence of the human  
XX AA  
XX aggrecanase protein of the invention  
XX AA  
XX Sequence 242 AA;  
XX AA  
XX Query Match 92.64; Score 1057; DB 5; Length 242;  
XX AA  
XX Best Local Similarity 100.04; Pred. No. 6e-102;  
XX AA  
XX Matches 200; Conservative 0; X mismatches 0; Indels 0; Gaps 0;  
XX AA

Qy 1 AAGGHLLELVANGVPDQVQNGESTERYVTNLGALLHDPSSLGAGFVHLVXVWIL 60  
Db 42 AAGGHLLELVANGVPDQVQNGESTERYVTNLGALLHDPSSLGAGFVHLVXVWIL 101  
Qy 61 TEPGAPNTANLTSLSVGGSGTINPDPDQALVLYTFHLELPQGNVRG 120  
Db 61 TEPGAPNTANLTSLSVGGSGTINPDPDQALVLYTFHLELPQGNVRG 120



CC coding regions of adint gene. Zints Polypeptides are used for tumour  
CC suppression, gene maturation, immunologic recognition, and growth and  
CC differentiation either working in isolation or in conjunction with other  
CC molecules in colon, small intestine, fetal lung, testis and placenta.  
CC treatment of disorders associated with recovery after gastrointestinal  
CC irradiation, chemotherapy or antibody use, as anti-infective, and  
CC use after radiation therapy and chemotherapy. The polypeptides also  
CC use after radiation therapy and chemotherapy. The polypeptides also  
CC cell adhesion, cell fusion and signalling. The polypeptides are also  
CC useful for treating tumour formation, Crohn's disease, inflammatory bowel  
CC disease, and other disorders. The polypeptides are also useful for  
CC immunology, trauma and epithelial disorders

XX Sequence 203 AA;  
SQ  
Query Match 91.74; Score 1046; DE 4; Length 203;  
Best Local Similarity 99.51; Pres. No. 6,66-101; Mismatches 0; Gaps 0;  
Matches 197; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QV 1 AAGGIIHELVAQVDFVQAGQEDTERTVLTNIGALLRPSLQAGFVRLVQVYL 60  
DB 1 AAGGIIHELVAQVDFVQAGQEDTERTVLTNIGALLRPSLQAGFVRLVQVYL 61  
QV 761 TFEQAPHTANTSSLSVQWQVQINPEDTDCGADLVMTFRDLEFDQNGQ 120  
DB 761 TFEQAPHTANTSSLSVQWQVQINPEDTDCGADLVMTFRDLEFDQNGQ 121  
QV 121 VTQAGASFTWCLIEDTDFDQVITAEIQRHGLEHDAQSGCQSGQVMAKKA 180  
DB 121 VTQAGASFTWCLIEDTDFDQVITAEIQRHGLEHDAQSGCQSGQVMAKKA 181  
QV 181 APRAGLAWFCSRQLLS 198  
DB 181 APRAGLAWFCSRQLLS 199

Search completed: March 13, 2004, 07:39:01  
Job time: 31.319 secs



Qy 181 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 214  
 Db 255 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 288

RESULT 2  
 US-09-836-712-2  
 ; Sequence 2, Application US/09816712  
 ; Patent No. US2001/004916A1  
 ; APPLICANT: PRISER INC.  
 ; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND  
 ; USES THEREOF  
 ; FILE REFERENCE: US/09-836,712  
 ; CURRENT APPLICATION NUMBER: US/09/836,712  
 ; PRIOR FILING DATE: 2001-04-17  
 ; SOFTWARE: Patent in Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1416  
 ; ORGANISM: Human  
 US-09-836-712-2

Query Match 100.0%; Score 1141; DB 9; Length 1416;  
 Best Local Similarity 100.0%; Pred. No. 5,4e-108;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 60  
 Db 98 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 157

Qy 61 TPEGQNPNTANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 120  
 Db 158 TPEGQNPNTANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 217

Qy 121 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 180  
 Db 218 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 277

Qy 181 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 214  
 Db 278 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 311

RESULT 3  
 US-10-222-334-2  
 ; Sequence 2, Application US/1022234  
 ; Patent No. US2001/0075110A1  
 ; APPLICANT: GINSBURG, David  
 ; APPLICANT: LEVY, Galina  
 ; APPLICANT: MORRIS, Silasbeth  
 ; TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof  
 ; FILE REFERENCE: UN-07288  
 ; CURRENT APPLICATION NUMBER: US/10/222,334  
 ; PRIOR FILING DATE: 2002-08-15 15:12.894  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1427  
 ; ORGANISM: Homo sapiens  
 US-10-222-334-2

Query Match 100.0%; Score 1141; DB 14; Length 1427;  
 Best Local Similarity 100.0%; Pred. No. 5,5e-108;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 60

Db 75 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 134

Qy 61 TPEGANANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 120  
 Db 135 TPEGANANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 194

Qy 121 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 180  
 Db 195 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 254

Qy 181 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 214  
 Db 255 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 288

RESULT 5  
 US-09-978-979-1  
 ; Sequence 1, Application US/0997899  
 ; Patent No. US2001/002102A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Racine, Lisa, A.  
 ; APPLICANT: Twine, Natalie, C.  
 ; APPLICANT: Wolfman, Neil  
 ; APPLICANT: Morris, Silasbeth  
 ; TITLE OF INVENTION: Aggracaine Molecules  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: American Home Products Corporation  
 ; STREET: One Campus Drive  
 ; CITY: Kew-Forest, New York  
 ; STATE: New Jersey

Query Match 100.0%; Score 1141; DB 14; Length 1427;  
 Best Local Similarity 100.0%; Pred. No. 5,5e-108;  
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 60  
 Db 75 AAGCTTLELLVANGPFOFQAGQDTERVYTNLNGALLRDPSSGACQFVHLVYVNTL 134

Qy 61 TPEGANANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 120  
 Db 135 TPEGANANTLSLSVCSQSTINPEDTDPGHADLVYITRFDLEPDQNRQVRG 194

Qy 121 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 180  
 Db 195 VTQGGASPTNSCLITETGDTGVTIAMEIGHSFGLHQAQSCGSGHMASDGA 254

Qy 181 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 214  
 Db 255 APFAGLANSFCSRRQLLSLSAGRCACVMDPPR 288

COUNTRY: USA  
 ZIP: 07054  
 COMPILED BY: J. B. BROWN  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: IBM PC compatible  
 SOFTWARE: PC-DOS/MS-DOS  
 RELEASE: 1.0, Version #1.30  
 CURRENT APPLICATION NUMBER: US/09/979,979  
 FILING DATE: 16-Oct-2001  
 PRIORITY: Unknown  
 PRIOR APPLICATION DATA: Unknown  
 APPLICATION NUMBER: US/60/241,469  
 FILING DATE: <Unknown>  
 ATTORNEY: NAME: Kapilov, Ellen J.  
 REGISTRATION NUMBER: 32,345  
 REFERENCE/DOCKET NUMBER: GI 5435P  
 TELEPHONE: (973) 660-5000  
 TELEFAX: (973) 683-4117  
 SEQUENCE: 242 amino acids  
 TYPE: amino acid  
 STRANDNESS: unknown  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Query Match 92.6%; Score 1057; DB 9; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 60  
 DB 42 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 101  
 QY 61 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 120  
 DB 102 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 161  
 QY 121 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 180  
 DB 162 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 221  
 QY 181 AFRAGLANSPCSRQLLSL 200  
 DB 222 AFRAGLANSPCSRQLLSL 241

RESULT 6  
 US-09-781-0808-1  
 Sequence 11, Application US/10057487  
 Publication No. US20010251361  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: Aggrucanase Molecules  
 CURRENT APPLICATION NUMBER: US/10/057,487  
 FILING DATE: 08/02/0073  
 PRIORITY: Unknown  
 PRIOR APPLICATION NUMBER: 60/241,469  
 NUMBER OF SEQ ID NOS: 8  
 SEQ ID NO: 1 Patent in Version 3.1  
 LENGTH: 242  
 TYPE: APT Homo sapiens  
 US-10-057-487-1

Query Match 92.6%; Score 1057; DB 14; Length 242;

Best Local Similarity 100.0%; Pred. No. 2.1e-100;  
 Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 60  
 DB 42 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 101  
 QY 61 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 120  
 DB 102 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 161  
 QY 121 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 180  
 DB 162 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 221  
 QY 181 AFRAGLANSPCSRQLLSL 200  
 DB 222 AFRAGLANSPCSRQLLSL 241

RESULT 7  
 US-09-781-0808-2  
 Sequence 11, Application US/097810808  
 Publication No. US20020142391  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides.  
 APPLICANT: HOLLAND, JIM  
 APPLICANT: SHEPPARD, PAUL  
 APPLICANT: VANAMOTO, GAYLE  
 TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides.  
 FILE REFERENCE: 99-82  
 CURRENT APPLICATION NUMBER: US/09/781,0808  
 CURRENT FILING DATE: 2002-01-30  
 PRIORITY: Unknown  
 SOFTWARE: PEST-SEQ for Windows Version 3.0  
 SEQ ID NO 2  
 LENGTH: 203  
 TYPE: APT Homo sapiens  
 US-09-781-0808-2

Query Match 95.7%; Score 1046; DB 9; Length 203;  
 Best Local Similarity 99.1%; Pred. No. 2.3e-99;  
 Matches 197; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 60  
 DB 2 AAGGTHLELLVAVGVDFQAHQEDTERVYLVNINIGALLRPSLGAQFRVHLVAVVIL 61  
 QY 61 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 120  
 DB 102 TPEQGNNTANTLSSLVCSQGTINPEDDTPGHADLVITRFPLEPQGNQVKG 121  
 QY 121 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 180  
 DB 162 VTQGLGACSPFNCLITDGTGLVTIAHIGSFLEHDAQPSGCGSRHWASDGA 191  
 QY 181 AFRAGLANSPCSRQLLSL 198  
 DB 182 AFRAGLANSPCSRQLLSL 199

RESULT 8  
 US-09-781-0808-11  
 Sequence 11, Application US/097810808  
 Publication No. US20020142391  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides.  
 APPLICANT: HOLLAND, JIM  
 APPLICANT: SHEPPARD, PAUL  
 APPLICANT: VANAMOTO, GAYLE  
 TITLE OF INVENTION: Anti-Angiogenic Intestinal Peptides.  
 FILE REFERENCE: 99-82

1 CURRENT APPLICATION NUMBER: US/09/781,080B  
 2 CURRENT FILING DATE: 2002-01-30  
 3 NUMBER OF SEQ ID NOS: 12  
 4 PRIORITY CLAIM: None  
 5 SEQ ID NO 1: Faceted for Windows Version 3.0  
 6 LENGTH: 1120  
 7 TYPE: PRT Homo sapiens  
 8 FEATURE:  
 9 NAME/KEY: VARIANT  
 10 LOCATION: (1120)  
 11 LOCATION INFORMATION: Aaa = Any Amino Acid  
 12 US-09-781-080B-11  
 13  
 14 Query Match 95.7% Score 1046 DB 9; Length 1120;  
 15 Best Local Similarity 100.0% Pred No. 1,8e-71; Mismatches 0; Indels 0; Gaps 0;  
 16  
 17 GENERAL INFORMATION:  
 18 APPLICANT: Laemmle, Bernhard  
 19 APPLICANT: Schefflinger, Friedrich  
 20 APPLICANT: Aroclite, Gerhard  
 21 APPLICANT: Kerschbäumer, Randolf  
 22 APPLICANT: Tagliavacca, Luigina  
 23 APPLICANT: Zimmermann, Klaus  
 24 APPLICANT: Purian, Miha  
 25 APPLICANT: Gerresen, Helena E.  
 26 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 27 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC  
 28 CURRENT APPLICATION NUMBER: US/09/833,328  
 29 CURRENT FILING DATE: 2001-04-12  
 30 PRIOR APPLICATION NUMBER: 09/721,254  
 31 PRIOR FILING DATE: 2000-11-22  
 32 NUMBER OF SEQ ID NOS: 15  
 33 SOFTWARE: Patent in version 3.1  
 34 SEQ ID NO 4  
 35 LENGTH: 148  
 36 TYPE: PRT  
 37 ORGANISM: human  
 38 US-09-833-328-4  
 39  
 40 Query Match 67.7% Score 773 DB 9; Length 148;  
 41 Best Local Similarity 100.0% Pred No. 1,8e-71; Mismatches 0; Indels 0; Gaps 0;  
 42  
 43 GENERAL INFORMATION:  
 44 APPLICANT: Laemmle, Bernhard  
 45 APPLICANT: Schefflinger, Friedrich  
 46 APPLICANT: Aroclite, Gerhard  
 47 APPLICANT: Kerschbäumer, Randolf  
 48 APPLICANT: Tagliavacca, Luigina  
 49 APPLICANT: Zimmermann, Klaus  
 50 APPLICANT: Purian, Miha  
 51 APPLICANT: Gerresen, Helena E.  
 52 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 53 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC  
 54 CURRENT APPLICATION NUMBER: US/09/833,328  
 55 CURRENT FILING DATE: 2001-04-12  
 56 PRIOR APPLICATION NUMBER: 09/721,254  
 57 PRIOR FILING DATE: 2000-11-22  
 58 NUMBER OF SEQ ID NOS: 15  
 59 SOFTWARE: Patent in version 3.1  
 60 SEQ ID NO 4  
 61 LENGTH: 148  
 62 TYPE: PRT  
 63 ORGANISM: human  
 64 US-09-833-328-4

65 1 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 66 155 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 67 165 VTQGGACSPMSCLTETDGFUGVTI 148  
 68 225 VTQGGACSPMSCLTETDGFUGVTI 148  
 69 181 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 70 285 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 71  
 72 RESULT 9  
 73 US-09-833-328-4  
 74 1 Sequence 4, Application US/0983328  
 75 2 Patent No. US20020367131A1  
 76 3 GENERAL INFORMATION:  
 77 4 APPLICANT: Laemmle, Bernhard  
 78 5 APPLICANT: Schefflinger, Friedrich  
 79 6 APPLICANT: Aroclite, Gerhard  
 80 7 APPLICANT: Kerschbäumer, Randolf  
 81 8 APPLICANT: Tagliavacca, Luigina  
 82 9 APPLICANT: Zimmermann, Klaus  
 83 10 APPLICANT: Purian, Miha  
 84 11 APPLICANT: Gerresen, Helena E.  
 85 12 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 86 13 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC  
 87 14 CURRENT APPLICATION NUMBER: US/09/833,328  
 88 15 CURRENT FILING DATE: 2001-04-12  
 89 16 PRIOR APPLICATION NUMBER: 09/721,254  
 90 17 PRIOR FILING DATE: 2000-11-22  
 91 18 NUMBER OF SEQ ID NOS: 15  
 92 19 SOFTWARE: Patent in version 3.1  
 93 20 SEQ ID NO 4  
 94 21 LENGTH: 148  
 95 22 TYPE: PRT  
 96 23 ORGANISM: human  
 97 24 US-09-833-328-4  
 98  
 99 Query Match 67.7% Score 773 DB 9; Length 148;  
 100 Best Local Similarity 100.0% Pred No. 1,8e-71; Mismatches 0; Indels 0; Gaps 0;  
 101  
 102 GENERAL INFORMATION:  
 103 1 APPLICANT: Laemmle, Bernhard  
 104 2 APPLICANT: Schefflinger, Friedrich  
 105 3 APPLICANT: Aroclite, Gerhard  
 106 4 APPLICANT: Kerschbäumer, Randolf  
 107 5 APPLICANT: Tagliavacca, Luigina  
 108 6 APPLICANT: Zimmermann, Klaus  
 109 7 APPLICANT: Purian, Miha  
 110 8 APPLICANT: Gerresen, Helena E.  
 111 9 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 112 10 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC

61 1 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 62 155 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 63 165 VTQGGACSPMSCLTETDGFUGVTI 148  
 64 225 VTQGGACSPMSCLTETDGFUGVTI 148  
 65 181 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 66 285 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 67  
 68 RESULT 10  
 69 US-09-833-328-5  
 70 1 Sequence 6, Application US/0983328  
 71 2 Patent No. US20020367131A1  
 72 3 GENERAL INFORMATION:  
 73 4 APPLICANT: Laemmle, Bernhard  
 74 5 APPLICANT: Schefflinger, Friedrich  
 75 6 APPLICANT: Aroclite, Gerhard  
 76 7 APPLICANT: Kerschbäumer, Randolf  
 77 8 APPLICANT: Tagliavacca, Luigina  
 78 9 APPLICANT: Zimmermann, Klaus  
 79 10 APPLICANT: Purian, Miha  
 80 11 APPLICANT: Gerresen, Helena E.  
 81 12 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 82 13 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC  
 83 14 CURRENT APPLICATION NUMBER: US/09/833,328  
 84 15 CURRENT FILING DATE: 2001-04-12  
 85 16 PRIOR APPLICATION NUMBER: 09/721,254  
 86 17 PRIOR FILING DATE: 2000-11-22  
 87 18 NUMBER OF SEQ ID NOS: 15  
 88 19 SOFTWARE: Patent in version 3.1  
 89 20 SEQ ID NO 4  
 90 21 LENGTH: 148  
 91 22 TYPE: PRT  
 92 23 ORGANISM: human  
 93 24 US-09-833-328-5  
 94  
 95 Query Match 67.7% Score 773 DB 9; Length 148;  
 96 Best Local Similarity 100.0% Pred No. 1,8e-71; Mismatches 0; Indels 0; Gaps 0;  
 97  
 98 GENERAL INFORMATION:  
 99 1 APPLICANT: Laemmle, Bernhard  
 100 2 APPLICANT: Schefflinger, Friedrich  
 101 3 APPLICANT: Aroclite, Gerhard  
 102 4 APPLICANT: Kerschbäumer, Randolf  
 103 5 APPLICANT: Tagliavacca, Luigina  
 104 6 APPLICANT: Zimmermann, Klaus  
 105 7 APPLICANT: Purian, Miha  
 106 8 APPLICANT: Gerresen, Helena E.  
 107 9 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 108 10 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC

61 1 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 62 155 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 63 165 VTQGGACSPMSCLTETDGFUGVTI 148  
 64 225 VTQGGACSPMSCLTETDGFUGVTI 148  
 65 181 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 66 285 AAGGILHELVANGPVFQAGQERTVNTNAGLRLPSLGAQGFVHLVWVIL 60  
 67  
 68 RESULT 11  
 69 US-09-833-328-5  
 70 1 Sequence 6, Application US/0983328  
 71 2 Patent No. US20020367131A1  
 72 3 GENERAL INFORMATION:  
 73 4 APPLICANT: Laemmle, Bernhard  
 74 5 APPLICANT: Schefflinger, Friedrich  
 75 6 APPLICANT: Aroclite, Gerhard  
 76 7 APPLICANT: Kerschbäumer, Randolf  
 77 8 APPLICANT: Tagliavacca, Luigina  
 78 9 APPLICANT: Zimmermann, Klaus  
 79 10 APPLICANT: Purian, Miha  
 80 11 APPLICANT: Gerresen, Helena E.  
 81 12 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 82 13 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC  
 83 14 CURRENT APPLICATION NUMBER: US/09/833,328  
 84 15 CURRENT FILING DATE: 2001-04-12  
 85 16 PRIOR APPLICATION NUMBER: 09/721,254  
 86 17 PRIOR FILING DATE: 2000-11-22  
 87 18 NUMBER OF SEQ ID NOS: 15  
 88 19 SOFTWARE: Patent in version 3.1  
 89 20 SEQ ID NO 4  
 90 21 LENGTH: 148  
 91 22 TYPE: PRT  
 92 23 ORGANISM: human  
 93 24 US-09-833-328-5  
 94  
 95 Query Match 67.7% Score 773 DB 9; Length 148;  
 96 Best Local Similarity 100.0% Pred No. 1,8e-71; Mismatches 0; Indels 0; Gaps 0;  
 97  
 98 GENERAL INFORMATION:  
 99 1 APPLICANT: Laemmle, Bernhard  
 100 2 APPLICANT: Schefflinger, Friedrich  
 101 3 APPLICANT: Aroclite, Gerhard  
 102 4 APPLICANT: Kerschbäumer, Randolf  
 103 5 APPLICANT: Tagliavacca, Luigina  
 104 6 APPLICANT: Zimmermann, Klaus  
 105 7 APPLICANT: Purian, Miha  
 106 8 APPLICANT: Gerresen, Helena E.  
 107 9 TITLE OF INVENTION: Compositing a von Willbrand Factor (vWF) Protease A  
 108 10 TITLE OF INVENTION: Compositing a Polypeptide Chain with the Amino Acid Sequence AAGC

FILE REFERENCES: 247, 0457  
CURRENT APPLICATION NUMBER: US/09/833,328  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 09/721,254  
PRIORITY DATE: 2001-04-11-22  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 15  
SEQ ID NO 16  
TYPE: PRT  
ORGANISM: human  
US-09-833-328-15  
Query Match  
Best Local Similarity: 100.0%; Pred.No. 1,26-65; Length 136;  
Matches 136; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;  
OY 13 AGPDVQAHQEDTERVLTNNGNELLRLPSGQAFVHVVWVLTPEGPATNLTN 72  
DB 1 AGPDVQAHQEDTERVLTNNGNELLRLPSGQAFVHVVWVLTPEGPATNLTN 60  
OY 73 LTSLSLVSGMSQTNEDDTPGHQALVLTFRDELPQNRQGVGTQZGACSPW 132  
DB 61 LTSLSLVSGMSQTNEDDTPGHQALVLTFRDELPQNRQGVGTQZGACSPW 120  
OY 133 SLCTEDTQFDLQVY 148  
DB 121 SLCTEDTQFDLQVY 136  
RESULT 12  
US-09-833-328-2  
Sequence 2, Application US/09833328  
Patent No. US20020136713A1  
GENERAL INFORMATION:  
APPLICANT: Schwan, Bernhard  
APPLICANT: Schwan, Bernhard  
APPLICANT: Scheiflinger, Friedrich  
APPLICANT: Arnone, Gerhard  
APPLICANT: Tschann, Michael  
APPLICANT: Tagliavacca, Humbold  
APPLICANT: Zimmermann, Klaus  
APPLICANT: Furlan, Miha  
APPLICANT: Gersten, Helena E.  
TITLE OF INVENTION: Composition Exhibiting a von Willebrand Factor (vWF) Protease Act  
TITLE OF INVENTION: Comprising a Polypeptide Chain with the Amino Acid Sequence AGG  
CURRENT APPLICATION NUMBER: US/09/833,328  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 09/721,254  
PRIORITY DATE: 2001-04-11-22  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 13  
SEQ ID NO 14  
TYPE: PRT  
ORGANISM: human  
US-09-833-328-2  
Query Match  
Best Local Similarity: 100.0%; Pred.No. 3,16-64; Length 133;  
Matches 133; Conservative: 0; Mismatches 0; Indels 0; Gaps 0;  
OY 16 PDVQAHQEDTERVLTNNGNELLRLPSGQAFVHVVWVLTPEGPATNLTN 75  
DB 1 PDVQAHQEDTERVLTNNGNELLRLPSGQAFVHVVWVLTPEGPATNLTN 60  
OY 76 SLVSGMSQTNEDDTPGHQALVLTFRDELPQNRQGVGTQZGACSPW 135  
DB 61 SLVSGMSQTNEDDTPGHQALVLTFRDELPQNRQGVGTQZGACSPW 120  
OY 136 LTEDTQFDLQVY 148

DB 121 LTEDTQFDLQVY 133  
RESULT 13  
US-09-831-151A-12  
Sequence 32, Application US/0981151A  
Publication No. US2003012256A1  
GENERAL INFORMATION:  
APPLICANT: Edinger, Shomit R  
APPLICANT: Gerlach, Valerie  
APPLICANT: MacDougall, John R  
APPLICANT: Smithson, Glenn X  
APPLICANT: Smithson, Glenn X  
APPLICANT: Millet, Isabelle  
APPLICANT: Peyman, John A  
APPLICANT: Smithson, Glenn X  
APPLICANT: Gunther, Erik  
APPLICANT: Ellerman, Karen  
APPLICANT: Shincere, Richard A  
APPLICANT: Gung'yi, Khalidamara  
APPLICANT: Guo, Xiaojia  
APPLICANT: Pattusajan, Veera  
APPLICANT: Taupier Jr, Raymond J  
APPLICANT: Zechusen, Bryan D  
APPLICANT: Kekuda, Rameeh  
APPLICANT: Szycki, Kimberly A  
APPLICANT: Smithson, Glenn X  
APPLICANT: Fernandes, Bina R  
APPLICANT: Gorman, Linda  
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same  
FILE REFERENCE: 214402-15C  
CURRENT APPLICATION NUMBER: US/09/81,151A  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 60/241,040  
PRIOR FILING DATE: 2000-10-21-24,1058  
PRIOR FILING DATE: 2000-10-17  
PRIOR FILING DATE: 2000-10-17  
PRIOR FILING DATE: 2000-10-17  
PRIOR FILING DATE: 2000-10-17  
PRIOR FILING DATE: 2000-10-17  
PRIOR FILING DATE: 2000-10-22,242,152  
PRIOR FILING DATE: 2000-10-22,242,152  
PRIOR FILING DATE: 2000-10-23  
PRIOR FILING DATE: 2000-10-23  
PRIOR FILING DATE: 2000-10-23,242,611  
PRIOR FILING DATE: 2000-10-23  
PRIOR FILING DATE: 2000-10-23  
PRIOR FILING DATE: 2000-10-23,242,680  
PRIOR FILING DATE: 2000-10-24  
PRIOR FILING DATE: 2000-10-24  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 32  
SEQ ID NO 37  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-891-151A-32  
Query Match  
Best Local Similarity: 31.6%; Score 361; DB 11; Length 997;  
Matches 87; Conservative 32; Mismatches 87; Indels 8; Gaps 5;  
OY 8 LELVAVGQVDFQAH--QEDTERVLTNNGNELLRLPSGQAFVHVVWVLTPEGA 66  
DB 244 VETVAVADARVETQVQVRSYVLTNNGNELLRLPSGQAFVHVVWVLTPEGA 303  
OY 67 PMTANLTSLSSVCGSNIPEDDTPGHQALVLTFRDELPQNR--QVETQVL 124

See File Wrapper or PALM.



Db 304 LXTHAANTLKSCCKKQKSNKKGDAFPHHTVATLLTKDL-CAMARPCETLGLSHV 362  
 QY 125 GKASCPWNCITETEDTQVLAETGSHGSLGQSGCGSG--HWASDGA 181  
 Db 363 AGMCQPHRCSINEDTGLPLAFVAHELHSGFQI QGDS-GNDCEPVKGRPPI MSPOLLY 421  
 QY 182 PHAGLWNSCGRQLLSLGSAGASQWPPP 212  
 Db 422 DAAPLTWNSCRQVITRELDGMLGLDDPP 452

Db 363 AGMCQPHRCSINEDTGLPLAFVAHELHSGFQI QGDS-GNDCEPVKGRPPI MSPOLLY 421  
 QY 182 PHAGLWNSCGRQLLSLGSAGASQWPPP 212  
 Db 422 DAAPLTWNSCRQVITRELDGMLGLDDPP 452

RESULT 15

US-09-918-171A-7  
 ; Sequence 7, Application US/09918171A  
 ; Patent No. US 6,700,109A1  
 ; INVENTOR: HURKALSEN, TITIA L.  
 ; APPLICANT: Apce. Sunneel  
 ; APPLICANT: HURKALSEN, TITIA L.  
 ; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
 ; FILE REFERENCE: 26473/04193  
 ; CURRENT APPLICATION NUMBER: US/09/918.171A  
 ; PRIOR APPLICATION NUMBER: 09/369,364  
 ; PRIOR FILING DATE: 1999-08-06  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 997  
 ; TYPE: PRT  
 ; NAME: Homo sapiens ADMPTS-7  
 ; US-09-918-171A-7

Query Match 31.6%; Score 360; DB 9; Length 997;  
 Best Local Similarity 38.4%; Pred. No. 1.2e-27;  
 Matches 81; Conservative 87; Mismatches 87; Gaps 5;

QY 9 ELLVAVDPVQNM-CEETERYVNTNIGALLRDLRPLQACFVRLVYVYVILTEGAP 67  
 Db 245 ELLVAVDANVYVGVQVSVYLLNNVAGLFDHPDIPNPHITVALLVLEDEEDL 304  
 QY 68 NITANLTSSLVCSGNTINFDPTDGHADVLTITRELELDPDS--QVQVTCGL 125  
 Db 305 KITHAANTLKSCCKKQKSNKKGDAFPHHTVATLLTKDL-CAMARPCETLGLSHV 363  
 QY 126 GKASCPWNCITETEDTQVLAETGSHGSLGQSGCGSG--HWASDGA 182  
 Db 364 GMCQPHRCSINEDTGLPLAFVAHELHSGFQI QGDS-GNDCEPVKGRPPI MSPOLLY 422  
 QY 183 PHAGLWNSCGRQLLSLGSAGASQWPPP 212  
 Db 423 DAAPLTWNSCRQVITRELDGMLGLDDPP 452

Search completed: March 13, 2004, 08:07:03  
 Job time : 17.9417 secs

Db 304 LXTHAANTLKSCCKKQKSNKKGDAFPHHTVATLLTKDL-CAMARPCETLGLSHV 362  
 QY 125 GKASCPWNCITETEDTQVLAETGSHGSLGQSGCGSG--HWASDGA 181  
 Db 363 AGMCQPHRCSINEDTGLPLAFVAHELHSGFQI QGDS-GNDCEPVKGRPPI MSPOLLY 421  
 QY 182 PHAGLWNSCGRQLLSLGSAGASQWPPP 212  
 Db 422 DAAPLTWNSCRQVITRELDGMLGLDDPP 452

RESULT 14

US-10-386-414-2  
 ; Sequence 2, Application US/10386414  
 ; Patent No. US 2004/006601A1  
 ; INVENTOR: KAPALLER, LIBERMAN, ROSINA  
 ; APPLICANT: Kapaller, Liberman, Rosina  
 ; APPLICANT: ROBINSON, KEITH E.  
 ; APPLICANT: ROBINSON, KEITH E.  
 ; APPLICANT: WILLIAMSON, MARK W.  
 ; APPLICANT: COOK, WILLIAM JAMES  
 ; APPLICANT: MEYERS, RACHEL E.  
 ; APPLICANT: CARROLL, JOSEPH M.  
 ; APPLICANT: CHUN, MYOUNG  
 ; TITLE OF INVENTION: 55925 ANT, 0218 MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: XP013-0210NMH  
 ; CURRENT APPLICATION NUMBER: US/10/386.414  
 ; PRIOR APPLICATION NUMBER: 09/436,282  
 ; PRIOR FILING DATE: 1999-10-25  
 ; PRIOR APPLICATION NUMBER: 09/436,282  
 ; PRIOR FILING DATE: 1999-10-25  
 ; PRIOR APPLICATION NUMBER: 09/330,970  
 ; PRIOR FILING DATE: 1999-06-11  
 ; PRIOR APPLICATION NUMBER: 09/724,599  
 ; PRIOR FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 09/660,193  
 ; PRIOR FILING DATE: 2001-05-16  
 ; PRIOR APPLICATION NUMBER: 10/093,023  
 ; PRIOR FILING DATE: 2001-10-31  
 ; PRIOR APPLICATION NUMBER: 10/010,943  
 ; PRIOR FILING DATE: 2000-12-07  
 ; PRIOR APPLICATION NUMBER: 60/354,037  
 ; PRIOR FILING DATE: 2000-12-07  
 ; PRIOR APPLICATION NUMBER: 09/833,082  
 ; PRIOR FILING DATE: 2000-12-07  
 ; NUMBER OF SEQ ID NOS: 19  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 266  
 ; TYPE: PRT  
 ; NAME: Homo sapiens  
 ; ORGANISM: Homo sapiens  
 ; US-10-386-414-2

Query Match 31.6%; Score 361; DB 15; Length 1686;  
 Best Local Similarity 38.4%; Pred. No. 1.2e-27;  
 Matches 81; Conservative 35; Mismatches 97; Indels 8; Gaps 5;

QY 8 ELLVAVDPVQNM-CEETERYVNTNIGALLRDLRPLQACFVRLVYVYVILTEGAP 66  
 Db 244 ELLVAVDANVYVGVQVSVYLLNNVAGLFDHPDIPNPHITVALLVLEDEED 303  
 QY 67 NITANLTSSLVCSGNTINFDPTDGHADVLTITRELELDPDS--QVQVTCGL 124  
 Db 304 LXTHAANTLKSCCKKQKSNKKGDAFPHHTVATLLTKDL-CAMARPCETLGLSHV 362  
 QY 125 GKASCPWNCITETEDTQVLAETGSHGSLGQSGCGSG--HWASDGA 181



; APPLICANT: Zambronic, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: 664939981 Human Processes and Polynucleotides Encoding the S  
 ; FILE REFERENCE: LEX-0105-USA  
 ; CURRENT APPLICATION NUMBER: US/09/963,791  
 ; CURRENT FILING DATE: 2000-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1: 36  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-963-791-20

Query Match 28.5%; Score 325.5; DB 4; Length 356;  
 Best Local Similarity 36.4%; Pred. No. 3.4e-27;  
 Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;  
 QY 8 LELLVANGVDVQAFQ-DEETERYVITNIGAEILADPSLGAQFVRLVVMVITPEGA 66  
 DB 101 VETLVADQVGVGVGKEDIEYLVNVIKALYRDSLVNVIIVAEIVLITDQ-- 158  
 QY 67 PNITAN-LTSSLSYVCONSQT---NPEDDTP---GHADVLYITRFDL---ELPD 113  
 DB 159 PNLIEHADSLSDFCKWQKLSHQSDNTIPENGADHNAVLTVDICTYKPK 218  
 QY 114 GNRGVQVQLGACSPFWSCLITDQGLVVIHIGESFRLDGAQSPGCPSP 173  
 DB 219 G---TLGLASVANGCEPSSINEDILGSAFTINEGINFNHNOI--GNSQTKGH 274  
 QY 174 ----VMSDGAAPAGLAMPSPQRLLSLGSAQRCV-MDPPA 213  
 DB 275 EAAKMAHITANTNPPNSACSDEYITFSLDSBGTCGLDNEPK 319

RESULT 3  
 ; Sequence 22, Application US/09963791  
 ; Patent No. 6649399  
 ; APPLICANT: Doncho, Gregory  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Scott, John  
 ; APPLICANT: Zambronic, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: No. 664939981 Human Processes and Polynucleotides Encoding the S  
 ; CURRENT APPLICATION NUMBER: US/09/963,791  
 ; CURRENT FILING DATE: 2000-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 22  
 ; LENGTH: 36  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-963-791-22

Query Match 28.5%; Score 325.5; DB 4; Length 438;  
 Best Local Similarity 36.4%; Pred. No. 4.4e-27;  
 Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;  
 QY 8 LELLVANGVDVQAFQ-DEETERYVITNIGAEILADPSLGAQFVRLVVMVITPEGA 66  
 DB 101 VETLVADQVGVGVGKEDIEYLVNVIKALYRDSLVNVIIVAEIVLITDQ-- 158  
 QY 67 PNITAN-LTSSLSYVCONSQT---NPEDDTP---GHADVLYITRFDL---ELPD 113  
 DB 159 PNLIEHADSLSDFCKWQKLSHQSDNTIPENGADHNAVLTVDICTYKPK 218

QY 114 GNRGVQVQLGACSPFWSCLITDQGLVVIHIGESFRLDGAQSPGCPSPGH 173  
 DB 219 G---TLGLASVANGCEPSSINEDILGSAFTINEGINFNHNOI--GNSQTKGH 274  
 QY 174 ----VMSDGAAPAGLAMPSPQRLLSLGSAQRCV-MDPPA 213  
 DB 275 EAAKMAHITANTNPPNSACSDEYITFSLDSBGTCGLDNEPK 319

RESULT 4  
 ; Sequence 10, Application US/09963791  
 ; Patent No. 6649399  
 ; APPLICANT: Doncho, Gregory  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Scott, John  
 ; APPLICANT: Zambronic, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: 664939981 Human Processes and Polynucleotides Encoding the S  
 ; CURRENT APPLICATION NUMBER: US/09/963,791  
 ; CURRENT FILING DATE: 2000-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 507  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-963-791-10

Query Match 28.5%; Score 325.5; DB 4; Length 507;  
 Best Local Similarity 36.4%; Pred. No. 5.8e-28;  
 Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;  
 QY 8 LELLVANGVDVQAFQ-DEETERYVITNIGAEILADPSLGAQFVRLVVMVITPEGA 66  
 DB 252 VETLVADQVGVGVGKEDIEYLVNVIKALYRDSLVNVIIVAEIVLITDQ-- 309  
 QY 67 PNITAN-LTSSLSYVCONSQT---NPEDDTP---GHADVLYITRFDL---ELPD 113  
 DB 310 PNLIEHADSLSDFCKWQKLSHQSDNTIPENGADHNAVLTVDICTYKPK 369  
 QY 114 GNRGVQVQLGACSPFWSCLITDQGLVVIHIGESFRLDGAQSPGCPSPGH 173  
 DB 219 G---TLGLASVANGCEPSSINEDILGSAFTINEGINFNHNOI--GNSQTKGH 425  
 QY 174 ----VMSDGAAPAGLAMPSPQRLLSLGSAQRCV-MDPPA 213  
 DB 426 EAAKMAHITANTNPPNSACSDEYITFSLDSBGTCGLDNEPK 470

RESULT 5  
 ; Sequence 12, Application US/09963791  
 ; Patent No. 6649399  
 ; APPLICANT: Doncho, Gregory  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Scott, John  
 ; APPLICANT: Zambronic, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: No. 664939981 Human Processes and Polynucleotides Encoding the S  
 ; CURRENT APPLICATION NUMBER: US/09/963,791  
 ; CURRENT FILING DATE: 2000-12-08  
 ; PRIOR FILING DATE: 1999-12-08  
 ; PRIOR FILING DATE: 1999-12-08

```

: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQUENCE: 24, Application US/09963791
: LENGTH: 589
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-963-791-12

      28.5%; Score 325.5; DB 4; Length 589;
Query Match
Best Local Similarity 36.4%; Pred. No. 12a-26;
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;

QY 8 LELLVAVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
DB 232 VETLVVADGVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
QY 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
DB 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
DB 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
DB 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
QY 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470
DB 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470

RESULT 6
US-09-963-791-24
: Sequence 24, Application US/09963791
: Patent No. 6649399
: ORGANISM: Homo sapiens
US-09-963-791-24

      28.5%; Score 325.5; DB 4; Length 589;
Query Match
Best Local Similarity 36.4%; Pred. No. 12a-26;
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;

: APPLICANT: Donobio, Gregory
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Friedlich, Glenn
: APPLICANT: Scoville, Brian
: APPLICANT: Zambrowski, Brian
: APPLICANT: Sands, Arthur T.
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6649399et Human Proteases and Polynucleotides Encoding the Sa
: CURRENT FILING DATE: 2000-12-08
: PRIOR FILING DATE: 2000-12-08
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-963-791-24

      28.5%; Score 325.5; DB 4; Length 589;
Query Match
Best Local Similarity 36.4%; Pred. No. 12a-26;
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;

QY 8 LELLVAVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
DB 101 VETLVVADGVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
QY 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
DB 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
DB 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
DB 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
QY 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470
DB 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470

RESULT 7
US-09-963-791-2
: Sequence 2, Application US/09963791
: Patent No. 6649399
: ORGANISM: Homo sapiens
US-09-963-791-2

      28.5%; Score 325.5; DB 4; Length 589;
Query Match
Best Local Similarity 36.4%; Pred. No. 12a-26;
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;

: APPLICANT: Donobio, Gregory
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Friedlich, Glenn
: APPLICANT: Scoville, Brian
: APPLICANT: Zambrowski, Brian
: APPLICANT: Sands, Arthur T.
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6649399et Human Proteases and Polynucleotides Encoding the
: CURRENT FILING DATE: 2000-12-08
: PRIOR FILING DATE: 2000-12-08
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 2
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-963-791-2

      28.5%; Score 325.5; DB 4; Length 589;
Query Match
Best Local Similarity 36.4%; Pred. No. 12a-26;
Matches 82; Conservative 36; Mismatches 82; Indels 25; Gaps 10;

QY 8 LELLVAVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
DB 232 VETLVVADGVGVDFQAH-QEDTERTVYVNIAGKLLDPSLGQFVWVWVLTTPSGA 66
QY 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
DB 67 PRITAN-LTSSLLVCSQMSQTI--NPEDDTP---GDAVLVITRFL---ELPD 113
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
DB 310 PLEINHAHNSLDFSCWKSLSHSGSONTIPENGIAHDAVLTIVCTIYNKFC 369
QY 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
DB 114 GNRQVGVYGLGACSPMSCLITETDQVLTAEIGASFLGHDGAPSGCPGSR 173
QY 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
DB 370 G---TGLASVADGAPAGLSPSCRLQLLSAGACV-WDPPR 213
QY 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470
DB 426 EAKMLAAHNTNTNFFSNACSDYITFDSGKGTCLNPPK 470

RESULT 8
US-09-963-791-2
: Sequence 4, Application US/09963792
: Patent No. 6448388
: ORGANISM: Homo sapiens
US-09-963-791-2

      27.0%; Score 307.5; DB 4; Length 1224;
Query Match
Best Local Similarity 36.2%; Pred. No. 1.9a-24;
Matches 77; Conservative 35; Mismatches 92; Indels 9; Gaps 5;

```



```

376 GTVCDSEKRSVIEDQLQAATTAIEIGHFIMFHMDKQACQKSLGWSGMMASMLLS 435
QY 178 --DGAAPRAGLAWSPCSRRGLLSLGRACRACWDPDR 213
DB 436 NLHSCP-----NSPCSAYNITSLFNGHGELDKQ 468

RESULT 12
US-09-563-791-16
; Sequence 16; Application US/0963791
; General Information:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedlich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sander, Arthur T.
; TITLE OF INVENTION: No. 6469396el Human Processes and Polynucleotides Encoding the Sa
; CURRENT APPLICATION NUMBER: US/09/563,791
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; NUMBER OF SEQ. NOS: 2-12-09
; NUMBER OF SEQ. NOS: 2-12-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: P
; ORGANISM: Homo sapiens
US-09-563-791-16

Query Match 36.4%; Score 303.; DB 4.; Length 317;
Best Local Similarity 36.5%; Pred. No. 14e-24;
Matches 77; Conservative 32; Mismatches 78; Indels 24; Gaps 9;

QY 8 LELUAVGDPDQVQVQDQETRYEYUJANIGELSLDSCGQAFVHUKVILTERCA 66
DB 101 VETVADNVRWQVQKQVQEHYLSLVNIVAKLVHSSGQVNIIVALLVLEIQ-- 158
QY 67 PNTAM--ITRSLVLSVGHQVQI-----NEEDPTQ---GHALVILVITFPL 118
DB 159 PNLNIMHAKSLDSCFKWKSLSHQQSDQTPENIAHEDNANIVITDICTVKNKFC 213
QY 114 GNRQGVGTGLGACSTFACILITPTQDPLQVTAHIGHAFSLHUGKSGQDSH 173
DB 219 G---TLLASVACVQCEESGNEIDLGSAFTIETGNGFNDQGI--GNSQGTGR 274

QY 174 ----VASDGAAPRAGLAWSPCSRRGLLSL 305
DB 275 EAKLVAAHITANTVPSFMAKSDYITSLF 305

```

```

1  RESULT 13
2  Sequence 6, Application: US-09-963-791-6
3  GENERAL INFORMATION:
4  APPLICANT: Donoho, Gregory
5  APPLICANT: Donoho, Alexander Jr.
6  APPLICANT: Friedlich, Glenn
7  APPLICANT: Friedlich, Glenn
8  APPLICANT: Scoville, John
9  APPLICANT: Sambowatz, Brian
10 APPLICANT: Sambowatz, Brian
11 APPLICANT: Sambowatz, Brian
12 TITLE OF INVENTION: NO. 6643959el Human Processes and polynucleotides encoding the sa
13 FILE REFERENCE: LEX-0108-USA
14 CURRENT APPLICATION NUMBER: US/09/963,791
15 PRIORITY APPLICATION NUMBER: US/09/963,791
16 PRIORITY APPLICATION NUMBER: US 67/169,769
17 PRIORITY FILING DATE: 1999-12-09
18 PRIORITY FILING DATE: 1999-12-09
19 SOFTWARE: FASTREC FOR Windows Version 4.0

```

[illegible][illegible]

## RESULT 15

US-09-800-729-155  
 : Sequence 155, Application US/09800729  
 : GENERAL INFORMATION:  
 : APPLICANT: NI et al.  
 : TITLE OF INVENTION: Human secreted proteins  
 : PUBLICATION NO: 2004-02045  
 : CURRENT APPLICATION NUMBER: US/09/800,729  
 : CURRENT FILING DATE: 2001-03-08  
 : PRIOR FILING DATE: 2000-09-22/US00/26013  
 : PRIOR APPLICATION NUMBER: 60/155,709  
 : PRIOR FILING DATE: 1999-09-24  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: Protein Ver. 2.0  
 : SEQ ID NO 155  
 : LENGTH: 2165  
 : ORGANISM: Homo sapiens

US-09-800-729-155

Query Match 35.81; Score 285; DB 4; Length 2165;  
 Best Local Similarity 30.44; Pval. No. 1e-22;  
 Matches 70; Conservative 30; Mismatches 104; Indels 26; Gaps 3;  
 QY 7 MLELLVNGPQVFGQSDTERVYLTNAGLELRUSLGHQFVHLVFWVLTPEGA 66  
 DB 281 YVELVADVTQNVETKRSLEDYLLFSTVASIYHQSLEASINVVYKLVLTENAG 340  
 QY 67 PNITANLSLLSVCHVSGTINPEDDTPQANLVYITSELPQHQGVGVYQLG 126  
 DB 341 PRITQAAQTQQPQVYVDPDSSVQHHVAILTRKIDCSQKCTITGLAELGT 400  
 QY 127 ACSPTNSGLITDCTFELQVITAEIGHGSGFLGHQAGPSGCGP ----- 170  
 DB 401 MCDMQSKALIEDNGLGAFTIANELHGVFISPHIDE--SKCSTMPVKYCFQSTED 458  
 QY 171 -----SCHVYAGDAGFAGLANSKESKROLLSL--SAGANVCVWPP 212  
 DB 455 KTFQNNHIVAPLTENTHPNSKSKAGMLEFLNNRQQTCLFQDP 508

Search completed: March 13, 2004, 07:46:06

Job time : 10.0281 secs

ON protein - protein search, using sw model

Run on: March 13, 2004, 07:33:19 ; Search time 2.4776 seconds

Title: US-09-036-712-2\_COPV\_124\_394

Sequences: 1 POLYUSNQCVRQFAPKAV.....VPLDQTEGVNWSKRC 71

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

283366

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Fred. No. is the number of results predicted by chance to have a  
maximum match of the same length as the query sequence printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	33.8	1205	218517	Procollagen N-pro
2	124.5	31.2	598	723536	hypothetical prote
3	121.5	30.5	921	700017	gene ADMP-1 prot
4	119.5	29.8	612	731198	hypothetical prote
5	117.5	29.8	612	731198	hypothetical prote
6	117.5	26.9	837	700155	hypothetical prote
7	101.5	25.4	1444	218866	angiogenesis inhib
8	74.5	18.7	810	707290	vascular apoptosis
9	74.5	18.7	810	707290	vascular apoptosis
10	73.5	18.4	997	718976	hypothetical prote
11	66.6	16.5	826	A60385	monocyte surface a
12	65.6	16.3	324	283529	Probable secretion
13	65.6	16.3	324	283529	Probable secretion
14	64.5	16.2	145	234574	Gene 70 protein -
15	64	16.0	549	949459	metallopeptinase
16	63.5	15.9	512	723454	metallopeptinase
17	63.3	15.9	512	723454	metallopeptinase
18	62.5	15.7	1042	723644	hypothetical prote
19	62	15.5	37	823403	sperm surface prot
20	62	15.5	37	823403	sperm surface prot
21	62	15.5	562	787207	phage-related prot
22	62	15.5	655	218623	disintegrin and ne
23	62	15.5	1113	218623	low-density lipopr
24	61.5	15.3	1620	218623	hypothetical prote
25	61.5	15.3	1620	218623	hypothetical prote
26	61	15.3	561	706518	probable H-transp
27	61	15.3	584	1 C6HUA	complement C8 alph
28	60.5	15.2	301	280984	hcn-like protein
29	60.5	15.2	301	280984	hcn-like protein
30	60.5	15.2	301	280984	hcn-like protein

## ALIGNMENTS

### RESULT 1

T18517  
 Procollagen N-endorpeptidase (EC 3.4.24.14) I - bovine  
 C:Species: Bos primigenius taurus (Cattle)  
 C:Date: 15-Oct-1999 Sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 Accession: T18517  
 Accession: T18517  
 Accession: T18517  
 A:Description: Cloning of the cDNA of the bovine procollagen I N-proteinase.  
 A:Reference number: 218941  
 A:Status: Preliminary; translated from GB/EML/DBSJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1205 <MW: 936389; NID:e990769; PID:e228215; PIDN:CAA65553.1  
 A:Experimental source: Skin  
 C:Genetic: C  
 A:Gene: PC I-NP  
 A:Description: catalyzes cleavage of the propeptides of type I and II collagens prior to  
 C:Keywords: hydrolase; metalloproteinase

Query Match 33.8% Score 139; DB 2; Length 1205;  
 Best Local Similarity 45.1%; Pred. No. 4,8e-07;  
 Matches 32; Conservative 5; Mismatches 32; Indels 2; Gaps 2;

QY 1 POLYUSNQCVRQFAPKAVCTAFAHLDNQALACHTDPDQSCSLLVPLDQTEC 60  
 DB 476 POLYUSNQCVRQFAPKAVCTAFAHLDNQALACHTDPDQSCSLLVPLDQTEC 533

QY 61 GVEVNSKRC 71

DB 534 APQKCFKNC 544

### RESULT 2

T23836  
 Hypothetical protein P57774 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 Sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 Accession: T23836  
 Accession: T23836  
 A:Reference number: 218623  
 A:Reference number: 218623  
 A:Accession: T23836  
 A:Status: Preliminary; translated from GB/EML/DBSJ  
 A:Residues: 1-506 <MW: 55811  
 A:Experimental source: Clone F57B7  
 C:Genetic: C



1 POLYTSANQVQVAFQKAVATFARSHLDQCA-SCHTDFDQSGSRLLVFLIDTTC 60  
 61 PDSYVDSNQVQVTFBDSRSEKFDPA--ASTCTLWGTSGGVVQCTKGFWDATGTC 117  
 61 GVEKWSKRC 71  
 118 GEGKGLNDR 128  
 RESULT 5  
 1. Species: Cnoroherbertia elegans  
 2. Species: Cnoroherbertia elegans  
 3. Date: 15-Oct-1999  
 4. Date: 15-Oct-1999  
 5. Date: 15-Oct-1999  
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 196. Date: 15-Oct-1999  
 197. Date: 15-Oct-1999  
 198. Date: 15-Oct-1999  
 199. Date: 15-Oct-1999  
 200. Date: 15-Oct-1999  
 201. Date: 15-Oct-1999  
 202. Date: 15-Oct-1999  
 203. Date:



Sal Mat 13 01:50:23 2007  
US 03 030 144 - 331.424  
US 03 030 144 - 331.424

[illegible]

C Species: Echis pyramidum leaky  
 C Accession: 548169  
 C Sequence Revision: 06-Dec-1996 #text\_change 09-Jun-2000  
 R Faine, M. J. I., Moura-De-Silva, A. M., Theakston, R. D. G., Crampston, J. M.  
 A Title: Cloning of metalloproteinase genes in the carpet viper (Echis pyramidum leaky).  
 A Reference number: 548160; MUID: 95010025; PMID: 7925163  
 A Accession: 548169  
 A Species: Echis pyramidum leaky  
 A Revision: 17549 <PAI>  
 A Cross-references: EMBL: X78971; NID: G763094; PIDN: CAA55566.1; PID: G763095  
 C Superfamily: mouse meltrin alpha; diintegrin homology  
 P 139-543/Domain: Propagide (segment); status Predicted <PRO>  
 F 139-543/Product: metalloproteinase H-II #status Predicted <MAT>  
 F 350-432/Domain: diintegrin homology <DIS>  
 F 1284/Active site: Glu #status predicted

Query Match 16.0%; Score 64; DB 2; Length 549;  
 Best Local Similarity 27.2%; Pred. No. 59;  
 Matches 25; Conservative 5; Mismatches 23; Indels 36; Gaps 6;  
 QY 10 QCRVAGPRV---AC-----TFAREHLM-----COASCHTDPLDS 45  
 DB 457 QCYAHQDAVQQAQCFINWCKGQFFCRKANDVTPQCBGVKCGKPEFEP---N 513  
 QY 46 SCSEILVPLD-----GTEGVKWCCKRC 71  
 DB 514 WCR---TFVGSQVDPGFKEDKXVCLDKRC 542

Search completed: March 13, 2004, 07:44:36  
 Job time : 3.4776 sec



[illegible]

Query Match 37.1%; score 148; DB 1; Length 1207;  
 least local similarity 39.4%; pred. No. 4.3e-09;

Lopez-Otin C.<sup>7</sup>  
RT  
Cloning, expression analysis, and structural characterization of  
PT  
several novel human annexin A family of metalloproteases with

Matches 28: Conservative 13; Mismatches 26; Indels 4; Gaps 3;

QY 1 POLYTSANQGVAPGPAVACTFAHRLDWALQCHDLPDQSCSLVLPDQTC 60  
DB 559 PONTYTDQCVLGLFGLAFQ-ENWY-ITGLQCKVE--GKSCRTLPDPMQTC 64  
DB 61 GYKWCMSKRC 71  
DB 615 DQMCVAC 625

RESULT 3  
AT19 MOUSE  
ID P15589 MOUSE STANDARD: PRT: 1310 AA.  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DE ADAMTS-19 precursor (M18; Antagonism of matrix metalloproteinase with thrombospondin motifs 19) (ADAM-TS19) (ADAM-TS19)  
GN ADAMTS19  
GN musculus (Mouse)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murus.  
CC NCBI\_TaxID:10093;  
CC SEQUENCE FROM N.A.

CC STRAIN=C57BL/6; TISSUE=Ovary;  
CC MEDLINE=2205168; PubMed=12617824;  
CC RefSeq=NM\_011953; Gene expression in the developing mouse gonad.;  
CC Gene Expr. Patterns 2:359-367(2002).  
CC -I- COPOLATOR: Binds 1 zinc ion per subunit (By similarity).  
CC -I- MATRIX (By similarity) secreted. Associated with the extracellular  
CC matrix (By similarity).

CC -I- TISSUE SPECIFICITY: Expressed predominantly in fetal ovary, low  
CC levels of expression is also detected in kidney, heart, skeletal  
CC muscle, and placenta.  
CC -I- DEVELOPMENTAL STAGE: Expression is strongest in anterior and  
CC ventral regions of the ovary at 12.5 and 13.5 dpc before becoming  
CC more uniform.

CC -I- ADAMTS-19 precursor is cleaved by a furin endopeptidase (By  
CC similarity).  
CC -I- SIMILARITY: Belongs to peptidase family M12B.  
CC -I- SIMILARITY: Contains 1 disintegrin-like domain.  
CC -I- SIMILARITY: Contains 1 P1AC domain.  
CC -I- SIMILARITY: Contains 1 P1AC domain.  
CC -I- CAUTION: By homology with the human sequence, it is uncertain  
CC whether Wec-1 or Wec-5 is the initiator.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use, but the copyright notice must be included in any redistribution.  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.ebi.ac.uk/submit/>  
CC or send an email to a license@ebi.ac.uk).  
CC ENBL: A1315193; AN101551.1;  
CC MCD; MG124428.5; Adant19.

CC InterPro: IPR006586; ADAM\_cysteine.  
CC InterPro: IPR001818; Pept\_M12A\_M12B.  
CC InterPro: IPR006025; Pept\_M\_Zn\_Bs.  
CC InterPro: IPR001590; Peptidase\_M12B.  
CC InterPro: IPR001590; Peptidase\_M12B.  
CC InterPro: IPR000844; TS1.  
CC Pfam: PF01562; Pept\_M12B\_propep; 1.  
CC Pfam: PF01421; Repolyglin; 1.  
CC SMART: SM00608; AKR1.1.  
CC SMART: SM00209; TSPI; 5.  
CC PROSITE: P550215; ADAM\_MERO; 1.

DR PROSITE: P550546; CYSTEINE SWITCH; FALSE NEG.  
DR PROSITE: P55027; DISINTEGRIN\_1; FALSE NEG.  
DR PROSITE: P55027; DISINTEGRIN\_2; FALSE NEG.  
DR PROSITE: P55050; PLAC\_1; FALSE NEG.  
DR PROSITE: P550092; TSPI; 5.  
DR PROSITE: P550447; ZINC-PROTEASE; 1.  
DR PROSITE: P550447; ZINC-PROTEASE; 1.  
KW Repeat: Extracellular matrix.  
FT SIGNAL 1 330 POTENTIAL  
FT CHIEP 330 1210 POTENTIAL  
FT CHIEP 330 1210 ADAMTS-19.  
FT DOMAIN 320 548 METALLOPROTEASE.  
FT DOMAIN 549 636 DISINTEGRIN-LIKE.  
FT DOMAIN 637 784 CYS-1.  
FT DOMAIN 637 784 CYS-1.  
FT DOMAIN 637 784 CYS-1.  
FT DOMAIN 784 947 SPACER.  
FT DOMAIN 948 978 TSP TYPE-1 2.  
FT DOMAIN 979 1042 TSP TYPE-1 4.  
FT DOMAIN 1042 1086 TSP TYPE-1 4.  
FT DOMAIN 1087 1147 TSP TYPE-1 5.  
FT DOMAIN 1163 1202 FLACINE SWITCH (POTENTIAL).  
FT DOMAIN 1163 1202 FLACINE SWITCH (POTENTIAL).  
FT METAL 485 485 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 486 486 ZINC (CATALYTIC) (BY SIMILARITY).  
FT METAL 489 489 ZINC (CATALYTIC) (BY SIMILARITY).  
FT CARBOHYD 490 490 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 491 491 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 263 263 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 800 800 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 931 931 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 931 931 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 952 952 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 1012 1012 N-LINKED (GLNAC) (POTENTIAL).  
FT CARBOHYD 1210 AA, 124560 AA, GMS1AANB15F32 C1647;  
QY Query Match 36.64; Score 146; DB 1; Length 1210;  
DB Best Local Similarity 39.44; Pred. No. 7.3e-05;  
DB Matches 28; Conservative 13; Mismatches 26; Indels 4; Gaps 3;  
QY 1 POLYTSANQGVAPGPAVACTFAHRLDWALQCHDLPDQSCSLVLPDQTC 60  
DB 562 PONTYTDQCVLGLFGLAFQ-ENWY-ITGLQCKVE--GKSCRTLPDPMQTC 617

DB 562 PONTYTDQCVLGLFGLAFQ-ENWY-ITGLQCKVE--GKSCRTLPDPMQTC 617  
QY 61 GYKWCMSKRC 71  
DB 618 DQMCVAC 625

RESULT 4  
ID A193193 N  
AC O15072; QMAN STANDARD: PRT: 1205 AA.  
DT 16-SEP-2003 (Rel. 40, Created)  
DT 16-SEP-2003 (Rel. 41, Created)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE ADAMTS-3 precursor (BC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAM-TS3) (ADAM-TS3)  
GN ADAMTS3 OR KIA03366  
GN musculus (Mouse)  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
CC NCBI\_TaxID:9606;  
CC SEQUENCE OF 1-227 FROM N.A.  
DE MEDLINE=2102912; PubMed=1460482;  
DE Fernandes A.J., Hirschata S., Engle J.M., Collie A., Cohn D.H.,  
DE Pfr Olligier M.S.,  
DE dermatopapillaria".  
DE J. Biol. Chem. 276:31502-31509 (2001).  
RL [2]



















[illegible]

Query March 32.19; Score 120; DB 1; Length 1911;

Best Local Similarity 36.6%; Pred. No. 1.3e-06;  
Matches 26; Conservative 8; Mismatches 33; Indels 4; Gaps 1;

1 POLYYSANEQCRVAFGPKAVACTPAREHIDMCQALSCHTDPDQCSCSRLLVPLLDGTEC 60

Db 479 DGRYDKNQCEIAFGPSQMC---PHINICNGLMCTSTEXLHKGCFTHVPPADGTC 534

Qy 61 GVEKWSKGRC 71

Db 535 GPGMHCRRHGLC 545

REPORT E 23

RESULTS 13  
ATSI RAT

ID	ATSL_RAT	STANDARD;	PRT; 967 AA.
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AC Q9WUQ1; Q9ERI1;

DT	16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last name=undead)

20-001-2001 (Ref. 40), first sequence update  
28-000-2003 (Ref. 41), last annotation update

DE ADAMTS-1 precursor (EC 3.4.24.-) (A diintegr

DE with thrombospondin motifs 1) (ADAM-TS 1) (A

GN ADAMTSI.  
CS PATTIE NORVEGIAN (PAT)

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata

CC Mammalia; Eutheria; Rodentia; Sciurognathi;

```

0X      NCBI_TaxID=10116;
0Y      /

```

RP SENTENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RA Liu X., Tu Y., Yin T., Johnstone E.M., Steph





















```

DR InterPro: IPRO00625; Sept_M_2n_BS.
DR InterPro: IPR00884; TSP1.
DR InterPro: IPR00895; TSP-1.
DR Pfam: PF00900; TSP1_1.
DR Pfam: PF00900; TSP1_2.
DR PRINTS: PR01705; TSP1REPEAT.
DR SMART: SMO068; ACR1.
DR SMART: SMO068; ACR2.
DR PROSITE: PS00132; ADAM_NEPHO.
DR PROSITE: PS00195; TSP1_3.
DR PROSITE: PS00142; ZINC_PROTEASE_1.
DR PROSITE: PS00142; ZINC_PROTEASE_2.
DR SEQUENCE 759 AA; 83410 MW; C18E8A0C4813C869 CRC64.

Query Match: 29.7% Score 148.5 DB: 6; Length 759;
Query Similarity: 29.7%; Expect 1e-436; Mismatch 3; Gaps 1
Matches 25; Conservative 5;

Oy 1 PELYNANERGVAFVAVATFAHEHLMQKASCHTDPQSSSLVPLLOTGC 60
Db 276 PGLYLVNRCQVFNGESGCEA--ASTCTLLTGSGLLVQTGFHFWDSTG 126

Oy 61 GGVWMSGRG 71
Db 327 GEGSMVNEKC 337

Search completed, March 13, 2004, 07:43:16
Job time : 8.02604 sec

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OS Hypothetical protein.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TaxID=9606.
XX [1]__TaxID=9606.
IN
SEQUENCE FROM N.A.
AP
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CC	XX	Fragment	227	PGLYTSENQCRVAFQVAVACTFAREHLMQALCHTDFLQSSCRSLVFLDQTC	286
CC	XX	Sequence 1353 AA;			
CC	XX	Query Match	100.04;	Score 399;	DB 5; Length 1353;
CC	XX	Best Local Similarity	100.04;	Pred. No. 38460;	
CC	XX	Matches	71;	Conservative	0; Mismatches
CC	XX	0; Gaps	0;		
CC	XX	1 POLYTSENQCRVAFQVAVACTFAREHLMQALCHTDFLQSSCRSLVFLDQTC	60		
CC	XX	227	PGLYTSENQCRVAFQVAVACTFAREHLMQALCHTDFLQSSCRSLVFLDQTC	286	
CC	XX	61	GVEMKSKGRC	71	
CC	XX	287	GVEMKSKGRC	297	
CC	XX	RESULT 4			
CC	XX	ID	ABB04153 standard; protein; 1416 AA.		
CC	XX	AA	ABB04153		
CC	XX	XX	ABB04153;		
CC	XX	XX	26-MAR-2002 (first entry)		
CC	XX	XX	Human ADAMTS-M polypeptide.		
CC	XX	XX	Osteoarthritis; rheumatoid arthritis; inflammatory bowel disease;		
CC	XX	XX	Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection;		
CC	XX	XX	myocardial infarction; atherosclerosis; congestive heart failure; myocardial infarction; stroke;		
CC	XX	XX	neurodegenerative disease; autoimmune disorder; Huntington's;		
CC	XX	XX	Parkinson's; migraine; pain; depression; multiple sclerosis; burn;		
CC	XX	XX	arteritis; diabetic retinopathy; gene therapy; thrombocytopenic purpura;		
CC	XX	XX	A disintegrin and metalloprotease, thrombospondin domain.		
CC	XX	XX	Homologous.		
CC	XX	XX	Key	Location/Qualifiers	
CC	XX	XX	1..97		
CC	XX	XX	/label=Prodomain		
CC	XX	XX	/note="The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain"		
CC	XX	XX	94..97		
CC	XX	XX	/label=Furin cleavage site		
CC	XX	XX	98..1416		
CC	XX	XX	/label=ADAMTS-M protein		
CC	XX	XX	/note="The mature form of the ADAMTS-M protein is processed by furin cleavage of the prodomain"		
CC	XX	XX	98..1416		
CC	XX	XX	/label=Metalloprotease domain		
CC	XX	XX	247..272		
CC	XX	XX	/label=Zinc-binding motif		
CC	XX	XX	324..394		
CC	XX	XX	/label=Disintegrin domain		
CC	XX	XX	418..431		
CC	XX	XX	/label=Thrombospondin submotif		
CC	XX	XX	432..424		
CC	XX	XX	/label=Heparin-binding domain		
CC	XX	XX	511..511		
CC	XX	XX	/label=Thrombospondin submotif		
CC	XX	XX	EP152055-A1.		
CC	XX	XX	07-NOV-2001.		
CC	XX	XX	27-APR-2001; 2001EP-0303706.		
CC	XX	XX	24-APR-2001; 2000US-0200040P.		
CC	XX	XX	(PFI2) PFIER PROD INC.		
CC	XX	XX	Buchbinder L, Mitchell PG, Neumann TS, Walsh RT.		
CC	XX	XX	WP: 2002-084275/12.		
CC	XX	XX	N-PSB; ABA02549.		
CC	XX	XX	New polynucleotide, useful in gene therapy, particularly for treating or		
CC	XX	XX	preventing e.g. arthritis, Crohn's disease, Alzheimer's disease and organ		
CC	XX	XX	transplant toxicity and rejection, comprises ADAMTS polynucleotide and		
CC	XX	XX	encoded polypeptide.		

QY 1 PGLYYSANEQCRVAFGPKAVACTFAREHLDMCQALSCHTDPLDQSSCSRLIVPLLDGTEC 60

[illegible]

















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; Patent No. US20040049106A1
; GENERAL INFORMATION:
; PRIORITY INFORMATION: PAPER: 6,924,469
; PRIORITY INFORMATION: PAPER: 6,924,469
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
; FILE REFERENCE: PLO851A
; PUBLICATION NO. US20030073116A1
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; LENGTH: 1416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-712-2

Query Match      100.0%; Score 399; DB 9; Length 1416;
Best Local Similarity 100.0%; Pred. No. 7,46-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 60
DB 324 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 383

QY 61 GVEKWCSCGRC 71
DB 384 GVEKWCSCGRC 394

RESULT 3
; Sequence 2
; Publication No. US20030073116A1
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Galia
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/10/222,334
; FILE REFERENCE: UN-07288
; CURRENT FILING DATE: 2002-09-16
; PRIORITY INFORMATION: PAPER: 6,924,469
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-222-334-2

Query Match      100.0%; Score 399; DB 14; Length 1427;
Best Local Similarity 100.0%; Pred. No. 7,46-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 60
DB 301 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 360

QY 61 GVEKWCSCGRC 71
DB 361 GVEKWCSCGRC 371

US-10-057-487-8
; Sequence 8
; Publication No. US2003010531A1
; APPLICANT: Ginsburg, David
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/10/057,487
; FILE REFERENCE: 08702.0073
; CURRENT FILING DATE: 2001-04-27

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; CURRENT FILING DATE: 2003-01-25
; GENERAL INFORMATION:
; PRIORITY INFORMATION: PAPER: 6,924,469
; PRIORITY INFORMATION: PAPER: 6,924,469
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
; FILE REFERENCE: PLO851A
; PUBLICATION NO. US20030073116A1
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-487-8

Query Match      100.0%; Score 399; DB 14; Length 1427;
Best Local Similarity 100.0%; Pred. No. 7,46-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 60
DB 331 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 360

QY 61 GVEKWCSCGRC 71
DB 361 GVEKWCSCGRC 371

RESULT 5
; Sequence 11
; Publication No. US20030073116A1
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Galia
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/09/781,080B
; FILE REFERENCE: 93-82
; CURRENT FILING DATE: 2002-01-30
; PRIORITY INFORMATION: PAPER: 6,924,469
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Pats-Seq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: VARIANT
; LOCATION: (11,1120)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-781-080B-11

Query Match      64.3%; Score 256; DB 9; Length 1120;
Best Local Similarity 72.0%; Pred. No. 7,1e-22;
Matches 59; Conservative 0; Mismatches 9; Indels 12; Gaps 3;

QY 2 GLYIANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 58
DB 331 GLYIANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 385

QY 59 EGVKWK---WCSKG 69
DB 386 EGVKWK---WCSKG 400

US-09-578-979-5
; Sequence 5
; Publication No. US2003010531A1
; APPLICANT: Ginsburg, David
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/09/578,979
; FILE REFERENCE: 08702.0073
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.1
; LENGTH: 1416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-487-8

Query Match      100.0%; Score 399; DB 9; Length 1416;
Best Local Similarity 100.0%; Pred. No. 7,46-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 60
DB 301 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 360

QY 61 GVEKWCSCGRC 71
DB 361 GVEKWCSCGRC 371

US-10-222-334-2
; Sequence 2
; Publication No. US20030073116A1
; APPLICANT: Ginsburg, David
; APPLICANT: Levy, Galia
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/10/222,334
; FILE REFERENCE: UN-07288
; CURRENT FILING DATE: 2002-09-16
; PRIORITY INFORMATION: PAPER: 6,924,469
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent in version 3.1
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-222-334-2

Query Match      100.0%; Score 399; DB 14; Length 1427;
Best Local Similarity 100.0%; Pred. No. 7,46-39;
Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 60
DB 301 POLYANEOQVARGPVAKVACTFAREHLMQCALSCHTDPDQSSCRLLVPLDITC 360

QY 61 GVEKWCSCGRC 71
DB 361 GVEKWCSCGRC 371

US-10-057-487-8
; Sequence 8
; Publication No. US2003010531A1
; APPLICANT: Ginsburg, David
; APPLICANT: Tsai, Han-Mou
; CURRENT APPLICATION NUMBER: US/10/057,487
; FILE REFERENCE: 08702.0073
; CURRENT FILING DATE: 2001-04-27

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1  NUMBER OF SEQUENCES: 6
2  CORRESPONDING SEQUENCE:
3  ADDRESSER: American Home Products Corporation
4  STREET: One Campus Drive
5  CITY: Parsippany
6  STATE: NJ
7  COUNTRY: USA
8  ZIP: 07054
9
10 COMPUTER READABLE FORM:
11 1. TITLE:
12 2. COMPUTER: IBM PC compatible
13 3. OPERATING SYSTEM: PC-DOS/MS-DOS
14 4. SOFTWARE: Patent Release #1.0, Version #1.10
15 5. CURRENT APPLICATION NUMBER: US/09/978,979
16 6. FILING DATE: 16-Oct-2001
17 7. PRIORITY CLAIM: Unknown
18 8. PRIOR APPLICATION NUMBER: US/60/241,469
19 9. FILING DATE: <Unknown>
20 10. ATTORNEY/AGENT INFORMATION:
21 11. REGISTRATION NUMBER: 32,345
22 12. REFERENCE/DOCKET NUMBER: 01 5435P
23 13. TELECOMMUNICATION INFORMATION:
24 14. TELEFAX: (973) 683-4117
25 15. INFORMATION FOR SEQ ID NO: 5:
26 16. SEQUENCE CHARACTERISTICS:
27 17. TYPE: amino acid
28 18. STRANDEDNESS: unknown
29 19. MOLECULE TYPE:
30 20. SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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US-10-188-869-4  
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 Matches 38; Conservative 7; Mismatches 20; Indels 8; Gaps 4;  
 1 POLYSIANQRVAGPVAVCTFAR--EHLDMQALSCHTDPLQSCSLVPLDPT 58  
 331 PGMHYSANEQQLFQNSA--TFCKNHHL-KAGDLWCLVE--GDTSCXKTLDPPLDPT 384  
 59 EGVGVKMSKRC 71  
 385 ECGAKMCKRAGEC 397  
 DB  
 385 ECGAKMCKRAGEC 397  
 DB  
 RESULT 10  
 US-10-188-869-4  
 ; Sequence 4, Application US/1018869  
 ; Publication No. US20030148306A1  
 ; GENERAL INFORMATION: EDWARD  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; TITLE OF INVENTION: AGGREGASE MOLECULES  
 ; FILE REFERENCE: 08702-0092-0000  
 ; CURRENT FILING DATE: 2002-07-05/188,869  
 ; PRIOR APPLICATION NUMBER: 60/349,133  
 ; PRIOR FILING DATE: 2002-01-16  
 ; PRIOR FILING DATE: 2001-06-05  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 807  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-188-869-4

Query Match 45.4%; Score 181; DB 14; Length 807;  
 Best Local Similarity 52.1%; Pred. No. 4.6e-13;  
 Matches 38; Conservative 7; Mismatches 20; Indels 8; Gaps 4;  
 1 POLYSIANQRVAGPVAVCTFAR--EHLDMQALSCHTDPLQSCSLVPLDPT 58  
 221 PGMHYSANEQQLFQNSA--TFCKNHHL-KAGDLWCLVE--GDTSCXKTLDPPLDPT 274  
 DB  
 59 EGVGVKMSKRC 71  
 275 ECGAKMCKRAGEC 287  
 DB

RESULT 11  
 US-10-188-869-10  
 ; Sequence 10, Application US/1018869  
 ; Publication No. US20030148306A1  
 ; GENERAL INFORMATION: EDWARD  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; TITLE OF INVENTION: AGGREGASE MOLECULES  
 ; FILE REFERENCE: 08702-0092-0000  
 ; CURRENT APPLICATION NUMBER: US/10188,869  
 ; CURRENT FILING DATE: 2002-07-05  
 ; PRIOR FILING DATE: 2002-01-16  
 ; PRIOR FILING DATE: 2001-06-05  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 807  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

US-10-188-869-10  
 Query Match 45.4%; Score 181; DB 14; Length 1057;  
 Matches 38; Conservative 7; Mismatches 20; Indels 8; Gaps 4;  
 1 POLYSIANQRVAGPVAVCTFAR--EHLDMQALSCHTDPLQSCSLVPLDPT 58  
 401 PGMHYSANEQQLFQNSA--TFCKNHHL-KAGDLWCLVE--GDTSCXKTLDPPLDPT 454  
 DB  
 59 EGVGVKMSKRC 71  
 455 ECGAKMCKRAGEC 467  
 DB  
 455 ECGAKMCKRAGEC 467  
 DB  
 RESULT 12  
 US-10-188-869-13  
 ; Sequence 13, Application US/1018869  
 ; Publication No. US20030148306A1  
 ; GENERAL INFORMATION: EDWARD  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; TITLE OF INVENTION: AGGREGASE MOLECULES  
 ; FILE REFERENCE: 08702-0092-0000  
 ; CURRENT APPLICATION NUMBER: US/10188,869  
 ; CURRENT FILING DATE: 2002-07-05/188,869  
 ; PRIOR APPLICATION NUMBER: 60/349,133  
 ; PRIOR FILING DATE: 2002-01-16  
 ; PRIOR FILING DATE: 2001-06-05  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1122  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-188-869-13

Query Match 45.4%; Score 181; DB 14; Length 1122;  
 Best Local Similarity 52.1%; Pred. No. 6.6e-13;  
 Matches 38; Conservative 7; Mismatches 20; Indels 8; Gaps 4;  
 1 POLYSIANQRVAGPVAVCTFAR--EHLDMQALSCHTDPLQSCSLVPLDPT 58  
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 DB  
 59 EGVGVKMSKRC 71  
 520 ECGAKMCKRAGEC 532  
 DB

RESULT 13  
 US-10-188-869-20  
 ; Sequence 20, Application US/1018869  
 ; Publication No. US20030148306A1  
 ; GENERAL INFORMATION: EDWARD  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: RACIE, LISA  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; APPLICANT: AGOSTINO, MICHAEL  
 ; TITLE OF INVENTION: AGGREGASE MOLECULES  
 ; FILE REFERENCE: 08702-0092-0000  
 ; CURRENT APPLICATION NUMBER: US/10188,869  
 ; CURRENT FILING DATE: 2002-07-05  
 ; PRIOR FILING DATE: 2002-01-16  
 ; PRIOR FILING DATE: 2001-06-05  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 20

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; LENGTH: 1145
; TYPE: BNT
; ORGANISM: Homo sapiens
US-10-057-489-20
54:44; Score 181; DB 14; Length 1145;
Query Match: 52.11; Pred. No: 6.7e-13;
Matches 38; Conservative 7; Mismatches 20; Indels 8; Gaps 4;

OY 1 POLY(AMINOACID)POLYMER-BUILDING BLOCKS FOR POLYMERIZATION
D 466 POLY(AMINOACID)POLYMER-BUILDING BLOCKS FOR POLYMERIZATION
D 59 ECTOGENS KRC 71
D 520 ECTOGENS KRC 332

RESULT 14
US 09-978-979-6
; Sequence 6, Application US/09978979
; Publication No. US20020151702A1
; GENERAL INFORMATION:
; APPLICANT: Twine, Natalie, C.
; Agostino, Michael, J.
; Wolfman, Elizabeth
; TITLE OF INVENTION: Aggracene Molecules
; NUMBER OF SEQUENCES: 6
; CORRESPONDING ADDRESS: Aggracene Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054

COMPUTER READABLE FORM:
; COMPUTER FILE: 09978979
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT INVENTION DATA:
; APPLICATION NUMBER: US/09/978,979
; FILING DATE: 16-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: US/60/241,469
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 32,345
; REGISTRATION NUMBER: 51,54359
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (973) 660-5000
; FAX: (973) 660-5417
; INFORMATION FOR SEQ ID NO: 6:
; LENGTH: 738 amino acids
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; NUCLEOTIDE SEQUENCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-978-979-6
38.11; Score 152; DB 9; Length 738;
Query Match: 52.11; Pred. No: 6.7e-13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 POLY(AMINOACID)POLYMER-BUILDING BLOCKS FOR POLYMERIZATION
D 153 POLY(AMINOACID)POLYMER-BUILDING BLOCKS FOR POLYMERIZATION

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RESULT 15
US 10-057-489-6
; Sequence 6, Application US/10057487
; Publication No. US2003010531A1
; GENERAL INFORMATION:
; APPLICANT: N/A
; TITLE OF INVENTION: Aggracene Molecules
; NUMBER OF SEQUENCES: 4
; FILE REFERENCE: 08702.0073 US/10/057,487
; CURRENT FILING DATE: 2001-10-21
; PRIOR APPLICATION NUMBER: 60/241,469
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ IDS: 4
; SOFTWARE: Protein version 3.1
; SEQ ID NO 6
; LENGTH: 738
; TOPOLOGY: unknown
; ORGANISM: homo sapien
; NAME/KEY: MISC FEATURE
; DESCRIPTION: (43)
; OTHER INFORMATION: unknown amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; DESCRIPTION: (115)
; OTHER INFORMATION: unknown amino acid
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; NAME/KEY: MISC FEATURE
; DESCRIPTION: (128)
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; OTHER INFORMATION: unknown amino acid
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US-10-057-489-6
38.11; Score 152; DB 14; Length 738;
Query Match: 52.11; Pred. No: 1.2e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GLYSYNSQCHVAFGFAFVACTFAREHL 29
D 153 GLYSYNSQCHVAFGFAFVACTFAREHL 180
Search completed: March 13, 2004, 08:07:04
Job time : 6.62093 secs

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OK protein - protein search, using sw model

Run on: March 13, 2004, 07:14:04 ; Search time 2.99511 Seconds  
(without alignments)  
1231727 Million cell updates/sec

Title: US-09-836-712-2\_COPY\_334\_394

Perfect score: 399

Sequence: 1 POLYUNIMODICVFQPVXV.....VELLDQGVGVNKSRC 71

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searchid: 389414 seqe, 51625971 residue

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : 1: Issued patents db.\*

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3: /cgm2\_6/prodata2/1aa/5B.COMB.psp.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SWMMARES

Result No.	Score	Query Match	Length	ID	Description
1	135	33.8	1211	4	US-09-491-522-5 Sequence 5, Appl
2	135	33.8	1211	4	US-09-491-522-5 Sequence 5, Appl
3	124.5	31.2	977	4	US-09-369-364A-2 Sequence 1, Appl
4	123	30.8	874	4	US-09-369-364A-1 Sequence 15, Appl
5	123	30.8	874	4	US-09-369-364A-1 Sequence 15, Appl
6	122	30.6	930	4	US-09-369-364A-2 Sequence 2, Appl
7	122	30.6	930	4	US-09-369-364A-2 Sequence 15, Appl
8	121.5	30.5	757	4	US-09-130-481-16 Sequence 15, Appl
9	121.5	30.5	757	4	US-09-130-481-16 Sequence 15, Appl
10	121.5	30.5	757	4	US-09-445-023A-12 Sequence 12, Appl
11	120.5	30.2	727	4	US-09-445-023A-1 Sequence 1, Appl
12	119.5	29.9	949	4	US-09-568-559-2 Sequence 1, Appl
13	119.5	29.9	949	4	US-09-568-559-2 Sequence 1, Appl
14	119.5	29.9	967	4	US-09-130-481-2 Sequence 2, Appl
15	117	29.3	318	4	US-09-369-364A-2 Sequence 15, Appl
16	117	29.3	318	4	US-09-369-364A-2 Sequence 15, Appl
17	111	27.8	2165	4	US-09-800-729-15 Sequence 15, Appl
18	109	27.3	1882	4	US-09-369-364A-1 Sequence 15, Appl
19	107.5	26.9	488	4	US-09-963-791-22 Sequence 2, Appl
20	107.5	26.9	488	4	US-09-963-791-22 Sequence 2, Appl
21	107.5	26.9	488	4	US-09-963-791-24 Sequence 24, Appl
22	107.5	26.9	837	4	US-09-132-1268-2 Sequence 2, Appl
23	107.5	26.9	837	4	US-09-132-1268-2 Sequence 2, Appl
24	107.5	26.9	837	4	US-09-634-286A-2 Sequence 2, Appl
25	96.5	24.2	1081	4	US-09-369-364A-17 Sequence 17, Appl
26	87.5	21.9	484	4	US-09-130-481-8 Sequence 8, Appl
27	77.5	19.4	905	4	US-09-369-364A-9 Sequence 9, Appl

28	66.5	16.7	859	4	US-09-369-364A-5 Sequence 5, Appl
29	66.5	16.7	859	4	US-09-369-364A-5 Sequence 5, Appl
30	65.5	16.4	595	4	US-09-352-991A-12406 Sequence 3406, A
31	62	15.5	1843	3	US-09-413-814-50 Sequence 50, Appl
32	62	15.3	594	1	US-09-113-288B-17 Sequence 17, Appl
33	60.5	14.6	116	1	US-08-139-862-4 Sequence 4, Appl
34	60.5	14.6	116	1	US-08-139-862-4 Sequence 4, Appl
35	60	15.0	269	1	US-08-203-716-3 Sequence 3, Appl
36	60	15.0	269	1	US-08-203-716-3 Sequence 3, Appl
37	60	15.0	269	1	US-08-440-179-3 Sequence 1, Appl
38	60	15.0	269	1	US-08-440-179-3 Sequence 1, Appl
39	60	15.0	269	2	US-08-483-806-2 Sequence 2, Appl
40	60	15.0	269	2	US-08-483-806-2 Sequence 2, Appl
41	60	15.0	269	1	US-09-211-290-11 Sequence 11, Appl
42	60	15.0	269	1	US-09-211-290-11 Sequence 11, Appl
43	60	15.0	269	3	US-09-039-657-3 Sequence 3, Appl
44	60	15.0	269	3	US-09-039-657-3 Sequence 3, Appl
45	60	15.0	269	3	US-08-748-547-11 Sequence 11, Appl
			269	3	US-09-486-030A-11 Sequence 11, Appl

# ALIGNMENTS

RESULT 1  
US-09-491-522-5  
Patent No. 642898  
GENERAL INFORMATION:  
APPLICANT: Colige, Alain  
INVENTOR: Colige, Alain  
APPLICANT: PROCOOP, Darwin J  
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,  
METHOD OF PRODUCTION AND USE THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESS: Penile & Edmunds, LLP  
STREET: 1195 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2211  
COMMODITY: BIOLOGICAL FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
CURRENT APPLICATION DATA: Windows Version 2.0b  
FILING DATE:  
APPLICATION NUMBER: US/09/491,522

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY: Abrams, Samuel B  
REGISTRATION NUMBER: 30,605  
REFERENCE/DOCUM NUMBER: 8399-0660-999  
TELEPHONE: 650-493-4915  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
SEQUENCE CHARACTERISTICS: 5  
LENGTH: 1211 amino acids  
TYPE: Polypeptide  
TOPOLOGY: Linear

US-09-491-522-5

Query Match 33.88, Score 135, DB 4, Length 1211,  
Best Local Similarity 45.11, Pred No. 50-08,  
Matches 32, Conservative 51, Mismatches 32, Indels 2.

QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 60  
DB 482 PELLVSNMLCRLDFGLGYNWCTAFRT-PDCKQALC-SUPDNYFCKTKGPPVLDVNC 539

DB 61 GVEWNSKGC 71  
DB 540 APOGNCFKGHC 950

RESULT 2  
US-09-350-872-4  
Query Match 33.8%; Score 135; DB 4; Length 1234;  
Best Local Similarity 39.4%; Pred. No. 9e-08;  
Matches 29; Conservative 9; Mismatches 31; Indels 4; Gaps 2;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 60  
DB 508 PELVDYDQVTCVQVGRALCMQDPKX-DICVLMCHR---IQKCYKFNANEGTIC 563

QY 61 GVEWNSKGC 71  
DB 564 GQWMCQKQC 574

RESULT 3  
US-09-369-364A-7  
Query Match 31.1%; Score 124; DB 4; Length 997;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 2;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 60  
DB 476 POLYSMDQCFDFGLGYNWCTAFRT-PDCKQALC-SHPDNYFCKTKGPPVLDVNC 533

QY 61 GVEWNSKGC 71  
DB 534 APOGNCFKGHC 544

RESULT 5  
US-09-369-364A-15  
Query Match 31.2%; Score 124; DB 4; Length 997;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 3;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 59  
DB 464 PVLVDYDQVTCVQVGRALCMQDPKX-DICVLMCHR---ITCHSKLNAVDTHT 515

QY 60 GVEWNSKGC 71

DB 516 GVEWNSKGC 527

RESULT 4  
US-09-491-522-11  
Query Match 31.1%; Score 124; DB 4; Length 1205;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 2;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 60  
DB 476 POLYSMDQCFDFGLGYNWCTAFRT-PDCKQALC-SHPDNYFCKTKGPPVLDVNC 533

QY 61 GVEWNSKGC 71  
DB 534 APOGNCFKGHC 544

RESULT 5  
US-09-369-364A-15  
Query Match 31.2%; Score 124; DB 4; Length 997;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 3;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 59  
DB 464 PVLVDYDQVTCVQVGRALCMQDPKX-DICVLMCHR---ITCHSKLNAVDTHT 515

QY 60 GVEWNSKGC 71

DB 516 GVEWNSKGC 527

RESULT 4  
US-09-491-522-11  
Query Match 31.1%; Score 124; DB 4; Length 1205;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 2;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 60  
DB 476 POLYSMDQCFDFGLGYNWCTAFRT-PDCKQALC-SHPDNYFCKTKGPPVLDVNC 533

QY 61 GVEWNSKGC 71  
DB 534 APOGNCFKGHC 544

RESULT 5  
US-09-369-364A-15  
Query Match 31.2%; Score 124; DB 4; Length 997;  
Best Local Similarity 43.7%; Pred. No. 1.1e-06;  
Matches 33; Conservative 5; Mismatches 33; Indels 2; Gaps 3;  
QY 1 POLYSANQCVAFQPMVACTFAREHLNMQALSCHTPDLQSCSLVPLVLOGTEC 59  
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QY 60 GVEWNSKGC 71

/ CURRENT FILING DATE: 1999-08-06  
 / NUMBER OF SEQ ID NOS: 31  
 / SOFTWARE: 1 Patent In Ver. 2.1  
 / LENGTH: 874  
 / TYPE: BPT  
 / ORGANISM: Mus musculus ADAMTS-9  
 US-09-369-364A-15

Query Match 30.6%; Score 122; DB 4; Length 930;  
 Best Local Similarity 33.8%; Pred. No. 1.4e-06;  
 Matches 24; Conservative 11; Mismatches 32; Indels 4; Gaps 1;

QY 1 POLYANISQGVAFGPKAVACTPAREHLDWQALSCHTDPLQSSCSRLVPLIGLQTEC 60  
 DB 487 FOOTDQTQCNLTFFGFSVVC---PMDVCARLCAVRCQWMLTKLPAVETPC 542

QY 61 GYENKSCRC 71  
 DB 543 GGRICLQRC 553

RESULT 8  
 US-09-634-286A-15  
 / Sequence 2, Application US/09634286A  
 / Patent No. 6521436  
 / APPLICANT: Bristol-Myers Squibb Company  
 / TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES  
 / FILE REFERENCE: DM6509A  
 / CURRENT APPLICATION NUMBER: US/09/634,286A  
 / CURRENT FILING DATE: 2000-08-09  
 / NUMBER OF SEQ ID NOS: 31  
 / SOFTWARE: Patent in version 3.0  
 / LENGTH: 930  
 / ORGANISM: Homo sapiens  
 US-09-634-286A-15

Query Match 30.6%; Score 122; DB 4; Length 930;  
 Best Local Similarity 33.8%; Pred. No. 1.4e-06;  
 Matches 24; Conservative 11; Mismatches 32; Indels 4; Gaps 1;

QY 1 POLYANISQGVAFGPKAVACTPAREHLDWQALSCHTDPLQSSCSRLVPLIGLQTEC 60  
 DB 487 FOOTDQTQCNLTFFGFSVVC---PMDVCARLCAVRCQWMLTKLPAVETPC 542

QY 61 GYENKSCRC 71  
 DB 543 GGRICLQRC 553

RESULT 9  
 US-09-130-491-16  
 / Sequence 16, Application US/09130491  
 / Patent No. 641001  
 / APPLICANT: Holtzman, Douglas A.  
 / TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
 / FILE REFERENCE: 0946/041001  
 / CURRENT APPLICATION NUMBER: US/09/130,491  
 / CURRENT FILING DATE: 1998-08-06  
 / EARLIER FILING DATE: 1998-08-06/059,108  
 / EARLIER FILING DATE: 1997-09-05  
 / EARLIER APPLICATION NUMBER: US 60/094,961  
 / NUMBER OF FILING DATES: 1997-08-06  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 15  
 / LENGTH: 931  
 / ORGANISM: Rattus rattus  
 US-09-130-491-16

Query Match 30.6%; Score 121.5; DB 4; Length 553;  
 Best Local Similarity 36.6%; Pred. No. 9.1e-07;  
 Matches 26; Conservative 4; Mismatches 38; Indels 3; Gaps 1;

QY 1 POLYANISQGVAFGPKAVACTPAREHLDWQALSCHTDPLQSSCSRLVPLIGLQTEC 60

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/ CURRENT FILING DATE: 1999-08-06  
 / NUMBER OF SEQ ID NOS: 31  
 / SOFTWARE: 1 Patent In Ver. 2.1  
 / LENGTH: 874  
 / TYPE: BPT  
 / ORGANISM: Mus musculus ADAMTS-9  
 US-09-369-364A-15

Query Match 30.8%; Score 123; DB 4; Length 874;  
 Best Local Similarity 35.2%; Pred. No. 1e-06; 34; Indels 4; Gaps 1;

QY 1 POLYANISQGVAFGPKAVACTPAREHLDWQALSCHTDPLQSSCSRLVPLIGLQTEC 60  
 DB 350 POLYVYVQVQLTIDSSQVTPYVQ---CRKNCNVQVQWQVCTHTPAAGTETC 405

QY 61 GYENKSCRC 71  
 DB 406 EGRKQKFCPC 416

RESULT 6  
 US-09-369-364A-2  
 / Sequence 2, Application US/09369364A  
 / Patent No. 6391610  
 / APPLICANT: Agnoscience Sunel  
 / APPLICANT: Ruckmalen, Tina L.  
 / TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
 / FILE REFERENCE: 2647/001016  
 / CURRENT APPLICATION NUMBER: US/09/369,364A  
 / CURRENT FILING DATE: 1999-08-06  
 / NUMBER OF SEQ ID NOS: 31  
 / SOFTWARE: Patent In Ver. 2.1  
 / SEQ ID NO 2  
 / LENGTH: 930  
 / ORGANISM: Mus musculus ADAMTS-5  
 US-09-369-364A-2

Query Match 30.6%; Score 122; DB 4; Length 930;  
 Best Local Similarity 33.8%; Pred. No. 1.4e-06;  
 Matches 24; Conservative 11; Mismatches 32; Indels 4; Gaps 1;

QY 1 POLYANISQGVAFGPKAVACTPAREHLDWQALSCHTDPLQSSCSRLVPLIGLQTEC 60  
 DB 487 FOOTDQTQCNLTFFGFSVVC---PMDVCARLCAVRCQWMLTKLPAVETPC 542

QY 61 GYENKSCRC 71  
 DB 543 GGRICLQRC 553

RESULT 7  
 US-09-122-126B-15  
 / Sequence 15, Application US/09122126B  
 / Patent No. 641001  
 / APPLICANT: Bristol-Myers Squibb Company  
 / TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES  
 / FILE REFERENCE: 0946/041001  
 / CURRENT APPLICATION NUMBER: US/09/122,126B  
 / CURRENT FILING DATE: 1998-07-24  
 / NUMBER OF SEQ ID NOS: 21  
 / SOFTWARE: Patent in version 3.0  
 / SEQ ID NO 15  
 / LENGTH: 930  
 / TYPE: BPT  
 / ORGANISM: Homo sapiens  
 US-09-122-126B-15

Db 62 POLYDANRCQFTGSESKPCDA---ASTCTLCTGTSGLLVGCVTKTRHFWALDGTSC 118  
 Query Match 30.5%; Score 121.5; DB 4; Length 727;  
 Best Local Similarity 36.6%; Pred. No. 1.2e-06;  
 Matches 26; Conservative 4; Mismatches 36; Indels 3; Gaps 1;  
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 Db 119 GGRMCVSKRC 129  
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 RESULT 10  
 US-09-445-023A-12  
 / Sequence 1; Application US/09445023A  
 / Patent No. 6565858  
 / GENERAL INFORMATION:  
 / APPLICANT: Hirose, Kunisaka  
 / APPLICANT: Hirose, Kunisaka  
 / APPLICANT: HAKOSAKI, Michinori  
 / APPLICANT: Ishioka, Keiko  
 / APPLICANT: Matsushita, Kouji  
 / APPLICANT: Kuno, Kouji  
 / TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
 / FILE REFERENCE: US095095023A  
 / CURRENT APPLICATION NUMBER: US/09/445,023A  
 / PRIOR FILING DATE: 1999-12-03  
 / PRIOR FILING DATE: 1997-06-03  
 / NUMBER OF SEQ ID NOS: 14  
 / SOFTWARE: Patent version 3.0  
 / SEQ ID NOS: 1-14  
 / LENGTH: 727  
 / TYPE: PRT  
 / ORGANISM: Mus sp.  
 US-09-445-023A-12  
 Query Match 30.5%; Score 121.5; DB 4; Length 727;  
 Best Local Similarity 36.6%; Pred. No. 1.2e-06;  
 Matches 26; Conservative 4; Mismatches 36; Indels 3; Gaps 1;  
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 Db 295 GGRMCVSKRC 305  
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 RESULT 11  
 US-09-445-023A-12  
 / Sequence 1; Application US/09445023A  
 / Patent No. 6565858  
 / GENERAL INFORMATION:  
 / APPLICANT: Hirose, Kunisaka  
 / APPLICANT: Inoguchi, Rii  
 / APPLICANT: HAKOSAKI, Michinori  
 / APPLICANT: Ishioka, Keiko  
 / APPLICANT: Matsushita, Kouji  
 / APPLICANT: Kuno, Kouji  
 / TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical  
 / FILE REFERENCE: US095095023A  
 / CURRENT APPLICATION NUMBER: US/09/445,023A  
 / PRIOR FILING DATE: 1999-12-03  
 / PRIOR FILING DATE: 1997-06-03  
 / NUMBER OF SEQ ID NOS: 14  
 / SOFTWARE: Patent version 3.0  
 / SEQ ID NOS: 1-14  
 / LENGTH: 727  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 US-09-445-023A-12

Query Match 30.3%; Score 120.5; DB 4; Length 727;  
 Best Local Similarity 36.6%; Pred. No. 1.6e-06;  
 Matches 26; Conservative 3; Mismatches 39; Indels 3; Gaps 1;  
 QY 1 POLYSANRCQVFARFQVAVACTFAREHDMQALSCHTDPLQSGRLVPLDGTSC 60  
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 Db 238 POLYDANRCQFTGSESKPCDA---ASTCTLCTGTSGLLVGCVTKTRHFWALDGTSC 294  
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 QY 61 GVEKMSKRC 71  
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 Db 285 GGRMCVSKRC 305  
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 RESULT 12  
 US-09-130-491-13  
 / Sequence 1; Application US/09130491  
 / Patent No. 6419974  
 / GENERAL INFORMATION:  
 / APPLICANT: Holtzman, Douglas A.  
 / TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83  
 / FILE REFERENCE: 0946/041001  
 / CURRENT APPLICATION NUMBER: US/09/130,491  
 / PRIOR FILING DATE: 1998-08-07  
 / EARLIER FILING DATE: 1997-09-05  
 / EARLIER FILING DATE: 1997-09-05  
 / EARLIER FILING DATE: 1997-08-06  
 / NUMBER OF SEQ ID NOS: 16  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NOS: 1-16  
 / LENGTH: 208  
 / TYPE: PRT  
 / ORGANISM: Mus musculus  
 US-09-130-491-13  
 Query Match 29.9%; Score 119.5; DB 4; Length 608;  
 Best Local Similarity 36.6%; Pred. No. 1.8e-06;  
 Matches 26; Conservative 3; Mismatches 39; Indels 3; Gaps 1;  
 QY 1 POLYSANRCQVFARFQVAVACTFAREHDMQALSCHTDPLQSGRLVPLDGTSC 60  
 |||||  
 Db 173 POLYDANRCQFTGSESKPCDA---ASTCTLCTGTSGLLVGCVTKTRHFWALDGTSC 228  
 |||||  
 QY 61 GVEKMSKRC 71  
 |||||  
 Db 230 GGRMCVSKRC 240  
 |||||  
 RESULT 13  
 US-09-565-559-2  
 / Sequence 1; Application US/09565559  
 / Patent No. 6649377  
 / GENERAL INFORMATION:  
 / APPLICANT: Kikuchi, Paul  
 / APPLICANT: Kikuchi, Paul  
 / APPLICANT: Heller, Renu  
 / APPLICANT: Van Wart, Harold  
 / TITLE OF INVENTION: Compositions of Polynucleotides, Polynucleotides, and Nucleic Acid  
 / FILE REFERENCE: ROCH-002  
 / CURRENT APPLICATION NUMBER: US/09/568,559  
 / PRIOR FILING DATE: 1999-05-10  
 / PRIOR FILING DATE: 1999-05-10  
 / PRIOR FILING DATE: 1999-05-10  
 / NUMBER OF SEQ ID NOS: 2  
 / SOFTWARE: Patent version 4.0  
 / SEQ ID NOS: 1-2  
 / LENGTH: 949  
 / TYPE: PRT  
 / ORGANISM: human  
 US-09-565-559-2

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Query March      29.3k | Score 117; DB 4 | Length 518;
Best Local Similarity 33.6k | Pred. No. 3e-06;
Matches 24; Conservative 9; Mismatches 34; Indels 4; Gaps 1;

QY 1 POLYANSGCQVFAPGKAVATVAREHMDLNCALSTDPDSCSBLVLLDTGEC 60
dbb 75 PQQDTQATQNNITGDFGVC---EKKDVCARLNCARVGGSCWLTCKLPAVEGTFC 130

QY 61 GYKESKQRC 71
dbb 131 GNGRCKQKCK 141

Search completed: March 13, 2004, 07:46:07
Job time : 3.99531 secs

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Search completed: March 13, 2004, 07:46:07  
Job time : 3.99511 sec



[illegible]







1 WSGHRSFCSACCGGCTTFRACCNHSAFGDCAVQGLQALQNCWTCQVETGLEW 60  
609 WWSG --ECSTCGGVGLACDGSFKNSSGKYVQGRBRYSNTGCPWUTGTPR 665  
61 SQCC 64  
666 EVCC 669

[illegible][illegible][illegible]

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      F:78-97/Domains: signal sequence #status predicted <SIG>  

      F:78-469/Product: propeptide #status experimental <MAT>  

      F:76-128/Domains: thrombospondin type 1 repeat homology <THR1>  

      F:73-52/Domains: thrombospondin type 1 repeat homology <THR2>  

      F:70-20/Domains: thrombospondin type 1 repeat homology <THR3>  

      F:65-33/Domains: thrombospondin type 1 repeat homology <THR4>  

      F:62-14/Domains: thrombospondin type 1 repeat homology <THR5>  

      F:57-40/Domains: thrombospondin type 1 repeat homology <THR6>  

      F:52-27/Domains: thrombospondin type 1 repeat homology <THR7>  

      F:47-20/Binding site: carbohydrate (Aun) [covalent] #status predicted  

      Query Match          39.9%   Score 145.5    DB 1 Length 469:  

      Genbank similarity   37.0%   E-value 1e-36   RefSeq  

      Local 26, Conservative  

      1 Gage 1:  
  

QY      1 MSWPEPSPSSGGGVVTRRQCNINFRAGACGADQAEKNTQ 50  

DB      139 NSGMWPEPSTVTSGKVTHRRQCNINFRAGCGH-FPGASGEANTQ 197  
  

RESULT 3  

C:Caenorhabditis elegans  

S:Caenorhabditis elegans  

C:Species Caenorhabditis elegans  

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000  

C:Accession:U01885; 12465  

C:Author:McIntyre A.  

C:Submitted to the EMBL Data Library, July 1995  

A:Reference number: Z:9021  

A:Accession:U01885  

A:Status: preliminary  

A:Molecule type: DNA  

A:Residues: 1-1444 <TRL>  

A:Cross-references: EMBL:Z50064; FDN:CA80293.1; GSPB:GN00026; CDSF:C02B4.1  

A:Source: Cloned cDNA  

A:McIntyre A.

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A-Reference number: Z8917  
A-Biosystem: Bacteria; Cyanobacteria  
A-Accession number: AF068062  
A-Status: preliminary; translated from GB/EMBL/DDBB  
A-Molecule type: DNA  
A-Sequence length: 336 bp  
A-Source: *Cyanospora nana*  
A-Cross-references: EMBL:ZS0006; FDN:CAA9302.1; GSPB:GN0028; CDSF:CQ284.1  
A-Experimental source: Clone TUC5  
A-Organism: *Cyanospora nana*  
A-Gene: CESP-QC284.1  
A-MAP position: X  
A-MAP coordinates: 25/3; 70/3; 96/3; 139/3; 187/1; 234/2; 282/3; 376/2; 422/2; 478/3; 509/3; 561/3  
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Query Mismatch: 19; Pct Ident: 50.018;  
Query GC: 52.5; Complementarity: 1;  
Query Gaps: 0; Complementarity: 1; Gaps: 1;

[illegible]









-1-	DOMAIN. The auxiliary domains including the TSPs domain, are required for specific extracellular localization and for its
-2-	varicose and aggrecanase activities.
-3-	PK. The precursor is cleaved by a furin endopeptidase (B
-4-	CC -1- SIMILARITY. Belongs to peptidase family M12A.
-5-	CC -1- SIMILARITY. Contains 1 disintegrin-like domain.
-6-	CC -1- SIMILARITY. Contains 1 GON domain.
-7-	CC -1- SIMILARITY. Contains 2 cysteine domains.
-8-	CC -1- SIMILARITY. Contains 2 cysteine domains.
-9-	CC This SWISS-PROT entry is copyright. It is produced through a collaboration
-10-	CC between the Swiss Institute of Bioinformatics and the EMBL outstation
-11-	CC in Grenoble. The copyright for this entry is held jointly by the two
-12-	CC institutions. The copyright for the data is held by the institution in no way
-13-	CC modified and this statement is not removed. Usage by and for commercial
-14-	CC entries requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
-15-	CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> )
-16-	CC
-17-	CC EMBL AF61918; AAF89106.1; -
-18-	CC EMBL AF48893; AAC15765.1; -
-19-	CC EMBL AF07733; BAA2550.1; -
-20-	CC EMBL AF07733; BAA2550.1; -
-21-	CC MEROPS: M12.021; -
-22-	CC
-23-	CC Genes: HNCN; HNCN2; ADAMTS9.
-24-	CC
-25-	CC EMBL AF61918; AAF89106.1; -
-26-	CC EMBL AF48893; AAC15765.1; -
-27-	CC EMBL AF07733; BAA2550.1; -
-28-	CC EMBL AF07733; BAA2550.1; -
-29-	CC MEROPS: M12.021; -
-30-	CC
-31-	CC Genes: HNCN; HNCN2; ADAMTS9.
-32-	CC
-33-	CC EMBL AF61918; AAF89106.1; -
-34-	CC EMBL AF48893; AAC15765.1; -
-35-	CC EMBL AF07733; BAA2550.1; -
-36-	CC EMBL AF07733; BAA2550.1; -
-37-	CC MEROPS: M12.021; -
-38-	CC
-39-	CC Genes: HNCN; HNCN2; ADAMTS9.
-40-	CC
-41-	CC EMBL AF61918; AAF89106.1; -
-42-	CC EMBL AF48893; AAC15765.1; -
-43-	CC EMBL AF07733; BAA2550.1; -
-44-	CC EMBL AF07733; BAA2550.1; -
-45-	CC MEROPS: M12.021; -
-46-	CC
-47-	CC Genes: HNCN; HNCN2; ADAMTS9.
-48-	CC
-49-	CC EMBL AF61918; AAF89106.1; -
-50-	CC EMBL AF48893; AAC15765.1; -
-51-	CC EMBL AF07733; BAA2550.1; -
-52-	CC EMBL AF07733; BAA2550.1; -
-53-	CC MEROPS: M12.021; -
-54-	CC
-55-	CC Genes: HNCN; HNCN2; ADAMTS9.
-56-	CC
-57-	CC EMBL AF61918; AAF89106.1; -
-58-	CC EMBL AF48893; AAC15765.1; -
-59-	CC EMBL AF07733; BAA2550.1; -
-60-	CC EMBL AF07733; BAA2550.1; -
-61-	CC MEROPS: M12.021; -
-62-	CC
-63-	CC Genes: HNCN; HNCN2; ADAMTS9.
-64-	CC
-65-	CC EMBL AF61918; AAF89106.1; -
-66-	CC EMBL AF48893; AAC15765.1; -
-67-	CC EMBL AF07733; BAA2550.1; -
-68-	CC EMBL AF07733; BAA2550.1; -
-69-	CC MEROPS: M12.021; -
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-71-	CC Genes: HNCN; HNCN2; ADAMTS9.
-72-	CC
-73-	CC EMBL AF61918; AAF89106.1; -
-74-	CC EMBL AF48893; AAC15765.1; -
-75-	CC EMBL AF07733; BAA2550.1; -
-76-	CC EMBL AF07733; BAA2550.1; -
-77-	CC MEROPS: M12.021; -
-78-	CC
-79-	CC Genes: HNCN; HNCN2; ADAMTS9.
-80-	CC
-81-	CC EMBL AF61918; AAF89106.1; -
-82-	CC EMBL AF48893; AAC15765.1; -
-83-	CC EMBL AF07733; BAA2550.1; -
-84-	CC EMBL AF07733; BAA2550.1; -
-85-	CC MEROPS: M12.021; -
-86-	CC
-87-	CC Genes: HNCN; HNCN2; ADAMTS9.
-88-	CC
-89-	CC EMBL AF61918; AAF89106.1; -
-90-	CC EMBL AF48893; AAC15765.1; -
-91-	CC EMBL AF07733; BAA2550.1; -
-92-	CC EMBL AF07733; BAA2550.1; -
-93-	CC MEROPS: M12.021; -
-94-	CC
-95-	CC Genes: HNCN; HNCN2; ADAMTS9.
-96-	CC
-97-	CC EMBL AF61918; AAF89106.1; -
-98-	CC EMBL AF48893; AAC15765.1; -
-99-	CC EMBL AF07733; BAA2550.1; -
-100-	CC EMBL AF07733; BAA2550.1; -
-101-	CC MEROPS: M12.021; -
-102-	CC
-103-	CC Genes: HNCN; HNCN2; ADAMTS9.
-104-	CC
-105-	CC EMBL AF61918; AAF89106.1; -
-106-	CC EMBL AF48893; AAC15765.1; -
-107-	CC EMBL AF07733; BAA2550.1; -
-108-	CC EMBL AF07733; BAA2550.1; -
-109-	CC MEROPS: M12.021; -
-110-	CC
-111-	CC Genes: HNCN; HNCN2; ADAMTS9.
-112-	CC
-113-	CC EMBL AF61918; AAF89106.1; -
-114	

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[illegible]







[illegible]

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Job time : 2.33333 secs

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Job time : 2.33333 secs





[illegible]









[illegible]

[illegible]

Query Match 44.1; Score 161; DB 5; Length 1091;  
Best Local Similarity 48.2; Pred. No. 4.8e-12;  
Matches 27; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

1 WSSWCPSPSPRS CGGGVTRRRQCNPRPAFGGRACVGADLQAEKNTQACEKQ 56  
662 WGPCKESESACGGGFRMRRECHDPA PUNGMECPGCRDYEENVCQSEVR 717

Search completed: March 13, 2004, 07:43:19  
Job time : 6.33333 secs





CC which inhibit the activity of the protein of the invention may have an  
 CC effect on the activity of the protein of the invention. The protein  
 CC (or fragment) may be used to develop inhibitors of aggregase, using  
 CC the structural analysis or computer-aided drug design. A  
 CC method which includes structural analysis or computer-aided drug design  
 CC degradation of aggregase. The invention may be useful for the development  
 CC of therapeutics for the treatment of aggregase-associated disorders.  
 CC of mutations in the nucleic acid sequence of the protein of the present  
 CC sequence is the amino acid sequence of the protein of the present  
 CC related to the human aggregase protein of the invention.

XX Sequence 365 AA;

Query Match 100.0%; Score 365; DB 7; Length 365;  
 Best Local Similarity 100.0%; Evid. NO. 3.3e-33; Indels 0; Gaps 0;  
 Matches 64; Conservative 0; Mismatches 0;

Oy 1 MSNSGPRFSCSGGVYTRQCNPPAFQGRACVGLADKQNTCAZCTQLDEM 60  
 Db 59 MSNSGPRFSCSGGVYTRQCNPPAFQGRACVGLADKQNTCAZCTQLDEM 118  
 Oy 61 500Q 64  
 Db 119 500Q 122

# RESULT 4

ID AU79217 standard; protein; 933 AA.

XX AU79217;

XX 15-JUL-2002 (first entry)

XX Human ADM-TS-like protein.

XX Human; ADM-TS-like protein; cardiovascular disorder; angina;  
 XX Human; ADM-TS-like protein; cardiovascular disorder; angina;  
 XX ischaemic heart disease; congestive heart failure; myocardial infarction;  
 XX ischaemic heart disease; arrhythmia; hypertensive vascular disease;  
 XX chronic peripheral arterial occlusive disease; acute arterial thrombosis;  
 XX inflammatory vascular disorder; chronic obstructive pulmonary  
 XX liver disorder.

XX Homo sapiens.

XX W020022699-A2.

XX 04-APR-2002.

XX 26-SEP-2001; 2001MO-EP0011124.

XX 28-SEP-2000; 2000US-0235881P.

XX 29-JUL-2001; 2001US-0307393P.

XX (FASB) BAYER AG.

XX Xiao Y;

XX MPI; 2000-383274/1.

XX N-P60B; ABX49356.

XX New Purified human ADM-TS-like protein, useful for identifying  
 XX modulators of protein activity for treating cardiovascular or liver  
 XX disorder or chronic obstructive pulmonary disease.

XX Claim 25; Fig 2; 106pp; English.

XX The invention relates to a human ADM-TS-like protein and the  
 XX polynucleotide encoding it. The protein of the invention is useful  
 XX for the treatment of ischaemic heart disease, congestive heart  
 XX vascular system, such as congestive heart failure, myocardial infarction,

CC ischaemic heart diseases (e.g., stable angina, unstable angina), atrial  
 CC fibrillation, congestive heart failure, chronic peripheral arterial  
 CC kinds of secondary arterial hypertension), and peripheral vascular  
 CC diseases (e.g., chronic peripheral arterial occlusive disease, acute  
 CC arterial thrombosis and embolism, intramural vessel disease).  
 CC are useful in diagnostic assays for detecting diseases and abnormalities  
 CC or susceptibility to disease and abnormalities related to the presence  
 CC of mutations in the nucleic acid sequence of the protein of the present  
 CC a disease condition. This sequence represents the human ADM-TS-like  
 CC protein

XX Sequence 933 AA;

Query Match 100.0%; Score 365; DB 5; Length 933;  
 Best Local Similarity 100.0%; Evid. NO. 3.3e-33; Indels 0;  
 Matches 64; Conservative 0; Mismatches 0;

Oy 1 MSNSGPRFSCSGGVYTRQCNPPAFQGRACVGLADKQNTCAZCTQLDEM 60  
 Db 330 MSNSGPRFSCSGGVYTRQCNPPAFQGRACVGLADKQNTCAZCTQLDEM 449  
 Oy 61 500Q 64  
 Db 450 500Q 453

# RESULT 5

ID A0016618

XX A0016618 standard; protein; 1397 AA.

XX A0016618;

XX 15-MAY-2003 (first entry)

XX Human von Willebrand factor (vWF)-cleaving enzyme-related protein #5.

XX Human; protease inhibitor; gene therapy; vWF-cleaving enzyme;  
 XX von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 XX platelet thrombosis; stenosis.  
 XX Homo sapiens.

XX W02002280356-A1.

XX 07-NOV-2002.

XX 25-APR-2002; 2002MO-JP004141.

XX 26-APR-2001; 2001JP-001284/2.

XX 27-JUL-2001; 2001JP-00227510.

XX 28-SEP-2001; 2001JP-00303977.

XX 25-JAN-2002; 2002JP-00017596.

XX (KAGA) CHENO-SBEO-THERAPEUTIC RES INST.

XX Sogajima K, Mima N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;

XX WPI; 2003-120479/11.

XX N-PS0B; ABT22884.

XX Claim 4; Page 93-101; 144pp; Japanese.

XX The invention comprises the amino acid and coding sequence of a von  
 XX Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 XX the von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
 XX developing drugs for e.g. myocardial infarction and cerebral infarction.

CC infection, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willebrand factor (vWF)-cleaving enzyme-related protein  
 QQ Sequence 1297 AA.

Query Match 100.0%; Score 365; DB 6; Length 1297;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30; Indels 0; Gaps 0;  
 Matches 64; Conservative 0; Mismatches 0

Oy 1 MSNSGPFSSRCSGGVVTERRQCNPRPAGGACVGLQDAEMONTQACETQLFEM 60  
 Db 313 MSNSGPFSSRCSGGVVTERRQCNPRPAGGACVGLQDAEMONTQACETQLFEM 372  
 Oy 61 SQQC 64  
 Db 373 SQQC 376

RESULT 6  
 ID AAO16620 standard; protein; 1343 AA.

XX Human von Willebrand factor (vWF)-cleaving enzyme-related protein #7.

XX Human, protease inhibitor; gene therapy; vWF-cleaving enzyme;

XX von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;

XX cerebral infarction; arteriosclerosis;

XX platelet thrombosis; stenosis.

XX Homo sapiens.

XX W0200288366-A1.

XX 07-NOV-2002.

XX 25-APR-2002; 2002MO-JP04141.

XX 26-APR-2001; 2001JP-00138142.

XX 27-JUL-2001; 2001JP-00227510.

XX 28-SEP-2001; 2001JP-00349777.

XX 25-JAN-2002; 2002JP-00017596.

XX (SAGA) CHEMO-SENSO-THERAPEUTIC RES INST.

XX Soejima K, Misura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;

XX WPI, 2003-120479/11.

XX N-PDBID; AB132566.

XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
 XX developing drugs for e.g. myocardial infarction and cerebral infarction.

Claim 4; Page 112-121, 144pp; Japanese.

XX The invention comprises the amino acid and coding sequence of a von  
 XX Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 XX thrombocytopenic purpura, and in developing drugs for myocardial  
 XX infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 XX and stenosis. The present amino acid sequence represents a human von  
 XX Willebrand factor (vWF)-cleaving enzyme-related protein

QQ Sequence 1293 AA;

Query Match 100.0%; Score 365; DB 6; Length 1321;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSNSGPFSSRCSGGVVTERRQCNPRPAGGACVGLQDAEMONTQACETQLFEM 60  
 Db 313 MSNSGPFSSRCSGGVVTERRQCNPRPAGGACVGLQDAEMONTQACETQLFEM 397  
 Oy 61 SQQC 64  
 Db 398 SQQC 401

RESULT 7  
 ID A0224449 standard; protein; 1353 AA.

XX A0224449;

XX 04-OCT-2002 (first entry)

XX Human von Willebrand factor-cleaving protease fragment #2.

XX Human; von Willebrand factor-cleaving protease; vWF-cp; therapy; enzyme;

XX transgenic animal; immunisation; thromboembolic disease; preeclampsia;

XX thrombosis; hemolytic uremic syndrome; hemolytic-uremic syndrome;

XX thrombotic thrombocytopenia; hemolytic-uremic syndrome;

XX transgenic; anticoagulant.

XX Homo sapiens.

XX M020024241-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-EP011391.

XX 22-NOV-2000; 2000US-08721254.

XX 12-APR-2001; 2001US-00433328.

XX (BAXT) BAXTER AG.

XX Lammle B, Gerritsen HE, Furlan M, Tusecek P, Schwarz H;

XX Scheifflinger F, Antoine G, Kerschbaumer R, Tagliavecchia L;

XX Zimmermann K, Voelkel D;

XX WPI; 2002-479950/51.

XX Novel isolated or substantially purified von Willebrand factor-cleaving

XX enzyme, which is useful for the treatment of thrombotic thrombocytopenic

XX thrombotic disease such as thrombotic thrombocytopenic purpura.

XX Claim 1; Page 64-69; 9pp; English.

XX The invention relates to an isolated or substantially pure von Willebrand  
 XX factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for  
 XX purifying vWF which involves providing a ligand under conditioning a  
 XX where vWF is bound to the ligand and recovering from the ligand purified  
 XX vWF. vWF-cp is useful for producing anti-vWF-cp polypeptide antibodies  
 XX which involve immunising a host animal with the vWF-cp. vWF-cp is useful for  
 XX producing a preparation of prophylaxis and therapy of thrombosis and  
 XX thromboembolic disease such as thrombotic thrombocytopenic purpura (TTP),  
 XX hemolytic uremic syndrome, preeclampsia, hemolytic-uremic syndrome or  
 XX plasmatic or coagulation-induced vWF. The invention is useful for  
 XX construction expression systems and generating transgenic animals which  
 XX express the polypeptide in vivo. The present sequence is human vWF-cp  
 XX fragment.

QQ Sequence 1353 AA;

Query Match 100.0%; Score 365; DB 5; Length 1353;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 60  
 DB 313 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 372  
 OY 61 SQQC 64  
 DB 373 SQQC 376

RESULT 8  
 AA016617  
 ID AAO16617 standard; protein; 1353 AA.  
 AC AAO16617;  
 XX  
 XX 15-MAY-2003 (first entry)  
 DE Human von Willebrand factor (vWF)-cleaving enzyme-related protein #4.  
 XX Humu; protease inhibitor; gene therapy; vWF-cleaving enzyme.  
 XX von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 CS Homo sapiens.  
 XX W0200288366-A1.  
 XX 07-NOV-2002.  
 PD 25-APR-2002; 2002MO-JP004141.  
 XX 25-APR-2001; 2001JP-00128342.  
 PR 27-JUL-2001; 2001JP-00227510.  
 PR 28-SEP-2001; 2001JP-00304577.  
 PR 25-JAN-2004; 2002JP-00017596.  
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
 PA Soejima K, Mimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;  
 XX WPI; 2003-120479/11.  
 XX N-PSDB; AB732593.  
 XX The invention comprises the amino acid and coding sequence of a von  
 CC Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 CC the invention are useful in the diagnosis and treatment of  
 CC thrombocytopenic purpura, and in developing drugs for myocardial  
 CC infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willebrand factor (vWF)-cleaving enzyme-related protein.  
 CC Claim 4; Page 82-92; 14pp; Japanese.  
 XX

Query Match 100.0%; Score 365; DB 6; Length 1353;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 60  
 DB 313 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 372  
 OY 61 SQQC 64  
 DB 373 SQQC 376  
 Query Match 100.0%; Score 365; DB 6; Length 1353;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 60  
 DB 313 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 372  
 OY 61 SQQC 64  
 DB 373 SQQC 376

RESULT 9  
 AA016619  
 ID AAO16619 standard; protein; 1378 AA.  
 AC AAO16619;  
 XX  
 XX 15-MAY-2003 (first entry)  
 DE Human von Willebrand factor (vWF)-cleaving enzyme-related protein #6.  
 XX Humu; protease inhibitor; gene therapy; vWF-cleaving enzyme.  
 XX von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 CS Homo sapiens.  
 XX W0200288366-A1.  
 XX 07-NOV-2002.  
 PD 25-APR-2002; 2002MO-JP004141.  
 XX 25-APR-2001; 2001JP-00128342.  
 PR 27-JUL-2001; 2001JP-00227510.  
 PR 28-SEP-2001; 2001JP-00304577.  
 PR 25-JAN-2004; 2002JP-00017596.  
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
 PA Soejima K, Mimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;  
 XX WPI; 2003-120479/11.  
 XX N-PSDB; AB732593.  
 XX The invention comprises the amino acid and coding sequence of a von  
 CC Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 CC the invention are useful in the diagnosis and treatment of  
 CC thrombocytopenic purpura, and in developing drugs for myocardial  
 CC infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,  
 CC and stenosis. The present amino acid sequence represents a human von  
 CC Willebrand factor (vWF)-cleaving enzyme-related protein.  
 CC Claim 4; Page 102-111; 14pp; Japanese.  
 XX  
 XX Sequence 1378 AA:  
 Query Match 100.0%; Score 365; DB 6; Length 1378;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 60  
 DB 313 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 397  
 OY 61 SQQC 64  
 DB 398 SQQC 401  
 Query Match 100.0%; Score 365; DB 6; Length 1416 AA.  
 Best Local Similarity 100.0%; Pred. No. 1.2e-30;  
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 60  
 DB 313 MSWSGPRSCSGGGVTRRCQNPFPFAFGACVADLAQENQNTACENTQLEFM 397  
 OY 61 SQQC 64  
 DB 398 SQQC 401  
 RESULT 10  
 AB04153  
 ID AB04153 standard; protein; 1416 AA.  
 AC AB04153;  
 XX  
 XX 25-MAR-2002 (first entry)  
 XX





Ft				1075.._ll3l	/note=/Thrombospondin type I motif"	
Dm	XX	XX	XX	W2020242441-42.		
Pd	XX	XX	XX	30-MAY-2002.		
Xf	XX	XX	XX	26-NOV-2001; 2001MO-EF013991.		
Pg	XX	XX	XX	23-NOV-2001; 2000US-00721254.		
Pg	XX	XX	XX	13-APR-2001; 2001US-0081328.		
Rn	XX	XX	XX	[BANT] ; BANTER AG.		
Rn	XX	XX	XX	Laemmle B., Gerritsen HE., Furian M., Turecek P., Schwarz H.; Pi Schallinger F., Antoine G., Kerschbaumer R., Tagliaavaca L; Pj Zimmermann A., Voelkel O;		
Dr	XX	XX	XX	N-FDSP; AMQ3532.		
Dr	XX	XX	XX	WP1: 2002-479950/S1.		
Pt	XX	XX	XX	Novel isolated or substantially purified Von Willbrand factor-cleaving Pt proteases, useful for producing preparation for therapy of thrombolysis and Pt thromboembolic disease such as thrombotic thrombocytopenic purpura.  Claim 1, Fig 5; 93pp; English.		
Cc	CC	CC	CC	The invention relates to an isolated or substantially pure von Willebrand Cc factor-cleaving protease (vWF-cp), polypeptide vWF-cp and method for Cc isolating said polypeptides from plasma by immunoprecipitation using a Cc solution comprising vWFcp and the polypeptide ligand under conditions Cc where vWF is bound to the ligand and recovering from the ligand purified Cc vWF-cp. vWF-cp is useful for producing anti-vWF-cp polypeptide antibodies Cc which are useful for treating thrombotic thrombocytopenic purpura-like Cc vWF cp polypeptide antibodies from the animal. vWF-cp is useful for Cc producing a preparation of prophylaxis and therapy of thrombolysis and Cc thromboembolic disease such as thrombotic thrombocytic purpura (TTP). Cc Hemolytic uremic syndrome. vWF-cp can also be used for processing Cc plasmas or recombinantly produced vWF. The invention is useful for Cc construction expression systems and generating transgenic animals which Cc express Polypeptides having the sequence of present invention. Cc protein. vWF-cp gene is located on chromosome 6p21.		
Sq	SS	SS	SS	Query Length 1427 AA;		
Sw	SW	SW	SW	Query Watch 100.0%; Score 365; DB 5; Length 1427; Seq Local Similarity 100.0%; Pred. No. 1,3e+30; Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	OY	OY	OY	1 MSNSPSGSGSRSCGGVVTRSEPCNNPPSPAGACVCNGLAENWCNTACTCEPLEM 60 387 MSNGSFGPRCSGSRCGGVVTRSEPCNNPPSPAGACVCNGLAENWCNTACTCEPLEM 60		
Db	DB	DB	DB	61 SQOC 64 447 SQOC 450		
Ds	DS	DS	DS	ADN94038		
Id	ID	ID	ID	ADN94038 standard; protein: 1427 AA.		
Ax	AX	AX	AX	ADN94038;		
Tt	TT	TT	TT	29-JAN-2004 (first entry)		
Hx	HX	HX	HX	Human aggrecanase protein amino acid sequence.		
Kw	KW	KW	KW	aggrecanase; aggrecan; articular cartilage; proteoglycan; proteolytic; Kw cartilage degradation; osteoarthritis; inflammatory joint disease; Kw aggrecan-associated disorder; osteorhritis; inflammatory condition; Kw aggrecanase associated disorder; osteorhitis; inflammatory condition;		

[illegible]



Search completed: March 13, 2004, 07:39:06  
Job time : 10.3667 secs



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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
    TYPE: amino acid
    STRANDEDNESS: unknown
    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-578-979-5
Query Match      100.0%; Score 365; DB 9; Length 365;
Best Local Similarity 100.0%; Pred. No. 2,8e-32;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 60
DB 59 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 118
QY 61 SQQC 64
DB 119 SQQC 122
DB 447 SQQC 450

RESULT 2
US-10-057-487-5
Query Match      100.0%; Application US/10057487
Publication No. US20030105131
GENERAL INFORMATION:
    APPLICANT: Wyeth
    FILE REFERENCE: 08702.0073
    CURRENT APPLICATION NUMBER: US/10/057,487
    PRIORITY FILING DATE: 2000-10-18
    PRIOR FILING DATE: 2000-10-18
    NUMBER OF SEQ ID NOS: 8
    SOFTWARE: Patent in version 3.1
    SEQ ID NO 1:
    SEQ ID NO 2:
    SEQ ID NO 3:
    SEQ ID NO 4:
    SEQ ID NO 5:
    SEQ ID NO 6:
    SEQ ID NO 7:
    SEQ ID NO 8:
    TYPE: PRT
    ORGANISM: homo sapiens
    FEATURES:
        NAME/KEY: MISC FEATURE
        OTHER INFORMATION: unknown amino acid
        NAME/KEY: MISC FEATURE
        LOCATION: [365]..[365]
    OTHER INFORMATION: unknown amino acid
US-10-057-487-5
Query Match      100.0%; Score 365; DB 14; Length 365;
Best Local Similarity 100.0%; Pred. No. 2,8e-32;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 60
DB 59 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 118
QY 61 SQQC 64
DB 119 SQQC 122
DB 447 SQQC 450

RESULT 3
US-10-057-487-5
Query Match      100.0%; Application US/10057487
Publication No. US20030105131
GENERAL INFORMATION:
    APPLICANT: Wyeth
    FILE REFERENCE: 08702.0073
    CURRENT APPLICATION NUMBER: US/10/057,487
    PRIORITY FILING DATE: 2000-10-18
    PRIOR FILING DATE: 2000-10-18
    NUMBER OF SEQ ID NOS: 8
    SOFTWARE: Patent in version 3.1
    SEQ ID NO 1:
    SEQ ID NO 2:
    SEQ ID NO 3:
    SEQ ID NO 4:
    SEQ ID NO 5:
    SEQ ID NO 6:
    SEQ ID NO 7:
    SEQ ID NO 8:
    TYPE: PRT
    ORGANISM: homo sapiens
    FEATURES:
        NAME/KEY: MISC FEATURE
        OTHER INFORMATION: unknown amino acid
        NAME/KEY: MISC FEATURE
        LOCATION: [365]..[365]
    OTHER INFORMATION: unknown amino acid
US-10-057-487-5
Query Match      100.0%; Score 365; DB 14; Length 365;
Best Local Similarity 100.0%; Pred. No. 2,8e-32;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 60
DB 59 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 118
QY 61 SQQC 64
DB 119 SQQC 122
DB 447 SQQC 450

RESULT 4
US-05-836-712-2
Query Match      100.0%; Application US/09836712
Publication No. US20010049106A
GENERAL INFORMATION:
    APPLICANT: PRIZER INC.
    FILE REFERENCE: 09072.0024
    CURRENT APPLICATION NUMBER: US/09/836,712
    PRIORITY FILING DATE: 2000-10-17
    PRIOR FILING DATE: 2000-10-17
    NUMBER OF SEQ ID NOS: 4
    SOFTWARE: Patent in Ver. 2.1
    SEQ ID NO 1:
    SEQ ID NO 2:
    SEQ ID NO 3:
    SEQ ID NO 4:
    TYPE: PRT
    ORGANISM: Human
US-05-836-712-2
Query Match      100.0%; Score 365; DB 9; Length 1416;
Best Local Similarity 100.0%; Pred. No. 1e-31;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 60
DB 410 WNSGSPSCSFGSGGVVTRQCNPPAFQGRACVAGLQAMNTOACETQLEPM 469

RESULT 5
US-10-222-334-2
Query Match      100.0%; Application US/1022334
Publication No. US2003007116A
GENERAL INFORMATION:
    APPLICANT: GlaxoSmithKline
    APPLICANT: Glaxo
    APPLICANT: Teal, Han-Mou
    TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
    CURRENT APPLICATION NUMBER: US/10/222,334
    PRIORITY FILING DATE: 2002-08-16
    PRIOR FILING DATE: 2002-08-16
    NUMBER OF SEQ ID NOS: 78
    SOFTWARE: Patent in version 3.1
US-10-222-334-2
Query Match      100.0%; Application US/1022334
Publication No. US2003007116A
GENERAL INFORMATION:
    APPLICANT: GlaxoSmithKline
    APPLICANT: Glaxo
    APPLICANT: Teal, Han-Mou
    TITLE OF INVENTION: ADAMTS13 Genes and Proteins and Variants, and Uses Thereof
    CURRENT APPLICATION NUMBER: US/10/222,334
    PRIORITY FILING DATE: 2002-08-16
    PRIOR FILING DATE: 2002-08-16
    NUMBER OF SEQ ID NOS: 78
    SOFTWARE: Patent in version 3.1

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; SEQ ID NO 2
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-070-5
Query Match 100.0%; Score 365; DB 14; Length 1427;
Best Local Similarity 100.0%; Pred No. 1e-31;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 60
DB 387 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 446

QY 61 SQQC 64
DB 447 SQQC 450

RESULT 6
US-10-017-487-8
; Sequence 6, Application US/1005487
; Publication No. US200301053141
; APPLICANT: AMGEN
; TITLE OF INVENTION: Aggriscanase Molecules
; FILE REFERENCE: 08702.0073
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 60/241,469
; PRIOR FILING DATE: 2000-10-18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1427
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-017-487-8
Query Match 100.0%; Score 365; DB 14; Length 1427;
Best Local Similarity 100.0%; Pred. No. 1e-31;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 60
DB 387 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 446

QY 61 SQQC 64
DB 447 SQQC 450

RESULT 7
US-10-014-070-5
; Sequence 5, Application US/10014070
; Publication No. US20020113955A1
; APPLICANT: AMGEN
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Curtis, Royce J Lynn
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 53014, A Human Metalloprotease Family
; FILE REFERENCE: 2001-11-13
; CURRENT FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSBO for Windows Version 4.0
; SEQ ID NO 1156
; LENGTH: 1156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-070-5
Query Match 100.0%; Score 206; DB 16; Length 1189;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 34; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 60
DB 558 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 617

RESULT 8
US-10-311-035-10
; Sequence 10, Application US/10311035
; Publication No. US20040021243A1
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: YUE, Henry
; APPLICANT: GANDHI, Anesha R.
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: DELIGNE, Angelle M.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: NEUFEN, Daniel B.
; APPLICANT: KATZ, David A.
; APPLICANT: HAFALIA, April
; APPLICANT: KHAN, Farish A.
; APPLICANT: CHAWLA, Navinder K.
; APPLICANT: LAO, Nongkai
; APPLICANT: LAO, Dyrong Aina M.
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AZIMWAI, Yalda
; APPLICANT: LU, Yan
; APPLICANT: ZAMKORAN, Jayalaxmi
; APPLICANT: REDDY, Roopa
; APPLICANT: DAS, Depotriya
; APPLICANT: KEANEY, Liam
; APPLICANT: TITLES OF INVENTION: Proteases
; FILE REFERENCE: PI-0123 PCT
; CURRENT APPLICATION NUMBER: US/10/311,035
; PRIOR APPLICATION NUMBER: 60/212,336; 60/213,956; 60/216,821; 60/218,941
; PRIOR FILING DATE: 2000-06-16; 2000-06-22; 2000-06-29; 2000-07-07; 2000-07-14
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-311-035-10
; NAME/KEY: misc feature
; FEATURE:
; ORGANISM: Homo sapiens
US-10-311-035-10
Query Match 100.0%; Score 206; DB 16; Length 1189;
Best Local Similarity 100.0%; Pred. No. 1e-120;
Matches 34; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 60
DB 558 MSNWPSFSCSGGVVTRRQCNPPAFGRACVGDQAQNCNTQACETQLPM 617
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Qy      61 SQQC 64
Db      618 AQQC 621

US-09-938-330-14
; Sequence 10, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1:
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-14
Query Match      56.4%; Score 206; DB 9; Length 1213;
Best Local Similarity 53.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy      61 SQQC 64
Db      618 AQQC 619

US-09-938-330-12
; Sequence 12, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12:
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-12
Query Match      56.4%; Score 206; DB 9; Length 1216;
Best Local Similarity 53.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy      61 SQQC 64
Db      618 AQQC 619

US-09-938-330-14
; Sequence 10, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1:
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-14
Query Match      56.4%; Score 206; DB 9; Length 1213;
Best Local Similarity 53.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy      61 SQQC 64
Db      618 AQQC 619

US-09-938-330-12
; Sequence 12, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12:
; LENGTH: 1216
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-12
Query Match      56.4%; Score 206; DB 9; Length 1216;
Best Local Similarity 53.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

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Qy      61 SQQC 64
Db      618 AQQC 618

US-09-938-330-10
; Sequence 10, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10:
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-938-330-10
Query Match      56.4%; Score 206; DB 9; Length 1219;
Best Local Similarity 53.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy      61 SQQC 64
Db      618 AQQC 618

US-09-938-330-8
; Sequence 8, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
US-09-938-330-8
; Sequence 8, Application US/09938330
; Patent No. US20020115838A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Scoville, John
; APPLICANT: Fridlie, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: NO. US20020115838A1 Human Proteases and Polynucleotides Encodin
; FILE REFERENCE: LEX-0237-USA US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR FILING DATE: 2000-09-19
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 8
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-712-2
Query Match      56.4%; Score 206; DB 9; Length 1222;
Best Local Similarity 51.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
1 MSGNGPSPSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 60
DB 555 NSMTWTFGSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 60
QY 61 SQQC 64
DB 615 AQQC 618
RESULT 13
US-10-014-070-2
; Sequence 2, Application US/10014070
; Publication No. US2002011955A1
; PATENT INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Spurling, Heidi Lynn
; APPLICANT: Spurling, Heidi Lynn
; TITLE OF INVENTION: 53034: A Human Metalloprotease Family
; TITLE OF INVENTION: Member and Uses Thereof
; FILE REFERENCE: US/00055333 (P.10)
; CURRENT FILING DATE: 2001-11-13 07/21, 070
; PRIOR APPLICATION NUMBER: 60/258,373
; PRIOR FILING DATE: 2000-12-22
; SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-070-2
Query Match      56.4%; Score 206; DB 13; Length 1223;
Best Local Similarity 51.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
1 MSGNGPSPSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 60
DB 555 NSMTWTFGSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 64
QY 61 SQQC 64
DB 615 AQQC 618
RESULT 14
US-10-205-368-4
; Sequence 2, Application US/10205368
; Publication No. US2003003262A1
; PATENT INFORMATION:
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: AGOSTINO, MICHAEL J.
; TITLE OF INVENTION: AGGREGANASE MOLECULES
; FILE REFERENCE: 08/02,0094-00000
; CURRENT APPLICATION NUMBER: US/10/205,368
; PRIOR APPLICATION NUMBER: 60/308,386
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/315,887
; PRIOR FILING DATE: 2001-08-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent Ver. 2.1
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; SEQ ID NO 4
; LENGTH: 1223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-368-4
Query Match      56.4%; Score 206; DB 14; Length 1223;
Best Local Similarity 51.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
1 MSGNGPSPSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 60
DB 555 NSMTWTFGSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 64
QY 61 SQQC 64
DB 615 AQQC 618
RESULT 15
US-09-938-330-18
; Sequence 18, Application US/09938330
; Publication No. US20011883A1
; PATENT INFORMATION:
; APPLICANT: Maize, D. Wade
; APPLICANT: Hilburn, Erin
; APPLICANT: Hilburn, Erin
; APPLICANT: Fiddler, John
; APPLICANT: Fiddler, John
; APPLICANT: Ro, Yi
; APPLICANT: Ro, Yi
; APPLICANT: Thirnes, C. Alexander Jr
; APPLICANT: Thirnes, C. Alexander Jr
; FILE REFERENCE: USX 0217, USA
; CURRENT APPLICATION NUMBER: US/09/938,330
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,104
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
; SEQ ID NO 18
; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-330-18
Query Match      56.4%; Score 206; DB 9; Length 1232;
Best Local Similarity 51.1%; Pred. No. 2.8e-14;
Matches 34; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
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DB 555 NSMTWTFGSCSGCGGVYTRCCNPPAFGGRACVADAGLQEMNTQKCEITLPEM 64
QY 61 SQQC 64
DB 615 AQQC 618
Job search completed: Match 13, 2004, 08:07:05
Job time : 5.0667 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OW protein - protein search, using sw model  
Run on: March 13, 2004, 07:34:04 / Search time 2.7 Seconds  
1233.727 Million cell updates/sec  
Title: US-09-836-712-2\_COPY\_410\_473  
Sequence: 1 NSKWPFSRSGGGVTVT.....EXCITACEKYLEMSQQC 64  
Scoring table: BIOSM22  
Gapop 13.0 , Gapext 0.5  
Searched: 389414 seqs, 5162971 residues  
Total number of hits satisfying chosen parameters: 389414  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Lifting first 45 summaries  
Database : 1: /cgm2\_6/prodata/2/ias/SA.COMB.pdp\*  
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4: /cgm2\_6/prodata/2/ias/SA.COMB.pdp\*  
5: /cgm2\_6/prodata/2/ias/ACTUS.COMB.pdp\*  
6: /cgm2\_6/prodata/2/ias/ACTUS.COMB.pdp\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	192	52.6	1284	4	US-09-930-872-4
2	183	50.1	1205	4	US-09-930-872-4
3	183	50.1	1205	4	US-09-930-872-4
4	179	49.0	874	4	US-09-369-364A-15
5	177	48.5	491	4	US-09-130-491-8
6	177	48.5	491	4	US-09-130-491-8
7	175	47.9	905	4	US-09-369-364A-9
8	165	45.2	1081	4	US-09-369-364A-17
9	162	44.4	1172	4	US-09-369-364A-19
10	162	44.4	1172	4	US-09-369-364A-19
11	161	44.1	930	4	US-09-369-364A-2
12	161	44.1	1170	1	US-08-13-2888-20
13	156	42.0	63	3	US-09-10-487-2
14	155	42.0	63	3	US-09-10-487-2
15	155	42.0	63	3	US-09-10-487-2
16	155	42.0	63	3	US-09-10-487-2
17	155	42.0	63	3	US-09-10-487-2
18	155	42.0	63	3	US-09-10-487-2
19	155	42.0	63	3	US-09-10-487-2
20	155	42.0	63	3	US-09-10-487-2
21	155	42.0	63	3	US-09-10-487-2
22	155	42.0	63	3	US-09-10-487-2
23	155	42.0	63	3	US-09-10-487-2
24	155	42.0	63	3	US-09-10-487-2
25	155	42.0	63	3	US-09-10-487-2
26	155	42.0	63	3	US-09-10-487-2
27	150.5	41.2	2165	4	US-09-800-729-155

ALIGNMENTS

RESULT 1  
US-09-930-872-4  
; Sequence 4, Application US/09930872  
; Patent No. 6448388  
; APPLICANT: Fiddle, Carl Johan  
; TITLE OF INVENTION: Human Proteases and Polynucleotides Encoding the  
; CURRENT APPLICATION NUMBER: US/09930872  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: US/60225,852  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1: 1224  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-930-872-4

Query Match 52.6%; Score 192; DB 4; Length 1224;  
Best Local Similarity 46.9%; Pred. No. 5.7e-13;  
Matches 30; Conservative 12; Mismatches 22; Indels 0; Gaps 0;  
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Db 589 NSKWPFSRSGGGVTVTTRCCNPPRAGCVGAGVGLACNCTACETOLEM 648  
Oy 61 SQCC 64  
Db 649 AAC 652  
RESULT 2  
US-09-369-364A-13  
; Sequence 13, Application US/0369364A  
; Patent No. 6391510  
; GENERAL INFORMATION:  
; APPLICANT: Hironaka, Tetsuo  
; APPLICANT: Hironaka, Tetsuo  
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
; CURRENT APPLICATION NUMBER: US/09369364A  
; CURRENT FILING DATE: 1999-08-06  
; NUMBER OF SEQ ID NOS: 31  
; SEQ ID NO 13: 1882  
; LENGTH: 1882

28 146 45.0 60 1 US-07-546-531D-12  
Sequence 12, Appl  
Patent No. 546100  
30 146 40.0 60 6 542E10-12  
Sequence 15, Appl  
31 145.5 39.9 469 1 US-08-11-288B-15  
Sequence 5, Appl  
32 137.5 31.7 859 4 US-09-369-364A-5  
Sequence 7, Appl  
33 134 36.7 943 2 US-08-808-98A-7  
Sequence 7, Appl  
34 134 36.7 943 2 US-08-808-98A-7  
Sequence 7, Appl  
35 134 36.7 943 2 US-08-808-98A-7  
Sequence 21, Appl  
36 134 36.7 943 2 US-08-808-98A-7  
Sequence 21, Appl  
37 130 35.6 1156 3 US-08-596-08A-121  
Sequence 1, Appl  
38 130 35.6 1156 3 US-08-596-08A-121  
Sequence 1, Appl  
39 130 35.6 1156 3 US-08-596-08A-121  
Sequence 1, Appl  
40 128 34.8 1745 4 US-09-800-729-125  
Sequence 135, Appl  
41 127 34.8 1745 4 US-09-800-729-125  
Sequence 89, Appl  
42 127 34.8 1745 4 US-09-800-729-125  
Sequence 89, Appl  
43 125 34.2 898 2 US-08-808-98A-5  
Sequence 5, Appl  
44 125 34.2 898 2 US-08-808-98A-5  
Sequence 5, Appl  
45 125 34.2 898 3 US-09-106-902A-5  
Sequence 5, Appl



QY 61. SEQC 64  
DB 181 EQQC 184

RESULT 6  
US-09-491-522-5  
Sequence 5, Application US/09491522  
Patent No. 6428998  
GENERAL INFORMATION:  
APPLICANT: Colige, Alain  
APPLICANT: Colige, Alain  
APPLICANT: Prockop, David J.  
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 48.8%; Pred. No. 2.5e-11;  
Matches 29; Conservative 9; Mismatches 26; Indels 0; Gaps 0;  
QY 1 WMSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 564 WMSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 623

QY 61. SEQC 64  
DB 624 EQQC 627

RESULT 7  
US-09-369-364A-9  
Sequence 9, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 48.8%; Pred. No. 2.5e-11;  
Matches 29; Conservative 9; Mismatches 26; Indels 0; Gaps 0;  
QY 1 WMSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 564 WMSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 623

QY 61. SEQC 64  
DB 624 EQQC 627

RESULT 8  
US-09-369-364A-17  
Sequence 17, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

RESULT 9  
US-09-369-364A-7  
Sequence 7, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

RESULT 10  
US-09-369-364A-4  
Sequence 4, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

RESULT 11  
US-09-369-364A-3  
Sequence 3, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

RESULT 12  
US-09-369-364A-2  
Sequence 2, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

RESULT 13  
US-09-369-364A-1  
Sequence 1, Application US/09369364A  
Patent No. 6391610  
GENERAL INFORMATION:  
APPLICANT: Apce, Suneal  
APPLICANT: Apce, Suneal  
APPLICANT: Hirohata, Sachio  
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases  
METHODS OF PRODUCTION, AND THE PRODUCTION, METHODS AND USES THEREOF  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds, LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
PUBLICATION NO.: 100948611  
COMPUTER SYSTEM: FORW.  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: MSO Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09491.522  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/886,333  
ATTORNEY/AGENT INFORMATION:  
NAME: Abrams, Samuel B.  
REGISTRATION NUMBER: 30,605  
TELEPHONE: 650-493-5556  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
ELECTRONIC MAIL ADDRESS:  
INFORMATION FOR SEQ ID NO. 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
STRANDNESS: single  
TOPOLOGY: linear  
US-09-491-522-5

Query Match  
Best Local Similarity 45.2%; Pred. No. 4.5e-10;  
Matches 27; Conservative 6; Mismatches 29; Indels 0; Gaps 0;  
QY 1 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 60  
DB 527 MSWPFSSCSGGVTRRCCNRPAPGACVAGLQASMTQACETKLEPM 586

QY 61. SEQC 64  
DB 587 EQQC 590

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: LENGTH: 397
: TYPE: PRT
: ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7
Query Match
: 44.7%; Score 161; DB 4; Length 397;
: Best Local Similarity 46.9%; Pred. No. 6.9e-10;
Matches 30; Conservative 5; Mismatches 23; Indels 0; Gaps 0;
QY 1 WSGWSPGSCRSGGGVVTRQCNPRPAGGACVAGLQAMQNTQACETCLEPM 60
DB 541 WSGWSPGSCRSGGGVVTRQCNPRPAGGACVAGLQAMQNTQACETCLEPM 60
QY 61 SQQC 64
DB 601 HWC 604

RESULT 10 -2888-30
US-09-369-364A-7
: Sequence 19, Application US/08313288B
: Patent No. 5756502
: GENERAL INFORMATION:
: APPLICANT: Hurskainen, Tiina L.
: TITLE OF INVENTION: Nucleic Acid Encoding Zinc Metalloprotease
: FILE REFERENCE: 26473/4007/10-30-00
: CURRENT APPLICATION NUMBER: US/09/369,364A
: PRIORITY DATE: 2003-08-08
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: Patent In Ver. 2.11
: SEQ ID NO 2
: COUNTRY: USA
: CITY: New York
: STATE: New York
: ADDRESS: Cooper & Dunham LLP
: ZIP: 10036
: COMPUTER READABLE FORM:
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
: APPLICATION NUMBER: US/08/313,288B
: FILING DATE: January 5, 1995
: REGISTRATION NUMBER: 28,678
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0526
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 172 amino acids
: STANDARDS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-313-288B-19
Query Match
: 44.4%; Score 162; DB 1; Length 1172;
: Best Local Similarity 48.1%; Pred. No. 1e-09;
Matches 25; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 1 WSGWSPGSCRSGGGVVTRQCNPRPAGGACVAGLQAMQNTQAC 52
DB 497 WSGWSPGSCRSGGGVVTRQCNPRPAGGACVAGLQAMQNTQAC 548

RESULT 11 -364A-2
US-09-369-364A-7
: Sequence 2, Application US/09369364A
: Patent No. 6391610
: GENERAL INFORMATION:
: APPLICANT: Hurskainen, Tiina L.
: TITLE OF INVENTION: Nucleic Acid Encoding Zinc Metalloprotease
: FILE REFERENCE: 26473/4007/10-30-00
: CURRENT APPLICATION NUMBER: US/09/369,364A
: PRIORITY DATE: 2003-08-08
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: Patent In Ver. 2.11
: SEQ ID NO 2
: COUNTRY: USA
: CITY: New York
: STATE: New York
: ADDRESS: Cooper & Dunham LLP
: ZIP: 10036
: COMPUTER READABLE FORM:
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.30
: APPLICATION NUMBER: US/08/313,288B
: FILING DATE: January 5, 1995
: REGISTRATION NUMBER: 28,678
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0526
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1170 amino acids
: STANDARDS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-113-2885-20
Query Match
: 44.1%; Score 161; DB 1; Length 1170;
: Best Local Similarity 51.9%; Pred. No. 1.3e-09;

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Query Match 23.84; Score 82.5; DB 1; Length 1172;  
Identity 94; Conserved 7; Mismatches 6; Indels 7; Gaps 1;  
Matches 15; Conservative 4; Mismatches 4;

Qy 6 WMECSVSCDQIGRA-----RFTCLQPMQ 30  
DB 390 WTCCSVTGSSTQHGSCDVTSTCLDSIQ 421

Search completed: March 13, 2004, 07:44:39  
Job time: 2.02396 secs

























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FT DOMAIN 875 879
FT ACT SITE 359 363
FT METAL 388 398
FT METAL 438 402
FT CARBOHYD 109 109
FT CARBOHYD 475 475
FT CARBOHYD 107 107
FT VARSPIC 1 68
FT VARSPIC 368 368
FT CONFLICT 868
FT CONFLICT 884 884
FT CONFLICT 923 923
FT CONFLICT 1024 1024
FT SEQUENCE 123 AA, 13387 SW, 3694AC409PFI7OF CMC64;
Query Match 27.3%; Score 94.5; DB 1; Length 123;
Best Local Similarity 33.3%; Pred. No. 0.0036;
Matches 21; Conservative 9; Mismatches 16; Indels 17; Gaps 3;
Oy 1 MHVTHMEGVSVCGLQRRDT-----LGRQAQFVPADPQHLKRVTVRCWAGP 54
Db 972 WLZGAWQCSCATCGSLQGVQVCRVNSLS-----WEG-DRIPTVQVCELA 1020
Oy Qy 55 CVG 57
Db 1021 CGG 1023
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Job time : 1.4083 sec

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Search completed: March 13, 2004, 07:39:57  
Job time : 1.20833 secs









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 OY 1 MWUWMECSVGGDQIGRRTCT-LQP-----QAQAQVADFCQ---HLKPV 45  
 DB 489 MWUWMECSVGGDQIGRRTCT-LQP-----QAQAQVADFCQ---HLKPV 45  
 RESULT 12  
 ID Q9UL17 PRELIMINARY; PRT: 1023 AA.  
 AC Q9UL17,  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein KIA1233 (Fragment).  
 GN KIA1233 (Homo).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 EX MEDLINE:14031619; PubMed:10571462; Hiroawa M, Nomura N, Ohara O,  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins." J Biol Chem 269:14515-14519, 1994.  
 DR ENEM; AB013059; BA06547.1; -.  
 DR InterPro; IPR001110; 19-like.  
 DR InterPro; IPR002884; 19-like.  
 DR Pfam; PF00647; 45; 3. 19-like.  
 DR Pfam; PF00090; tps1; 6.  
 DR SMART; SM0209; TSP1; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS0092; TSP1; 6.  
 DR NON\_TIR  
 RP SEQUENCE 1023 AA; 119521 MW; DQACFF6A0A5D0A1 CRG64;  
 Best Local Similarity 34.2%; Score 115; DB 4; Length 1023;  
 Matches 19; Conservative 6; Mismatches 28; Indels 0; Gaps 0;  
 OY 1 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
 DB 933 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
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 ID P22897 PRELIMINARY; PRT: 766 AA.  
 AC P22897,  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT Chabot-McCormick 2003 (TrEMBLrel. 23, Last annotation update)  
 GN ADAMTSL2, precursor (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 EX MEDLINE:14031619; PubMed:10571462; Hiroawa M, Nomura N, Ohara O,  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins." J Biol Chem 269:14515-14519, 1994.  
 DR ENEM; AB013059; BA06547.1; -.  
 DR InterPro; IPR001110; 19-like.  
 DR InterPro; IPR002884; 19-like.  
 DR Pfam; PF00647; 45; 3. 19-like.  
 DR Pfam; PF00090; tps1; 6.  
 DR SMART; SM0209; TSP1; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS0092; TSP1; 6.  
 DR NON\_TIR  
 RP SEQUENCE 1023 AA; 119521 MW; DQACFF6A0A5D0A1 CRG64;  
 Best Local Similarity 34.2%; Score 115; DB 4; Length 1023;  
 Matches 19; Conservative 6; Mismatches 28; Indels 0; Gaps 0;  
 OY 1 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
 DB 933 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
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 ID P22897 PRELIMINARY; PRT: 766 AA.  
 AC P22897,  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT Chabot-McCormick 2003 (TrEMBLrel. 23, Last annotation update)  
 GN ADAMTSL2, precursor (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 EX MEDLINE:14031619; PubMed:10571462; Hiroawa M, Nomura N, Ohara O,  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins." J Biol Chem 269:14515-14519, 1994.  
 DR ENEM; AB013059; BA06547.1; -.  
 DR InterPro; IPR001110; 19-like.  
 DR InterPro; IPR002884; 19-like.  
 DR Pfam; PF00647; 45; 3. 19-like.  
 DR Pfam; PF00090; tps1; 6.  
 DR SMART; SM0209; TSP1; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS0092; TSP1; 6.  
 DR NON\_TIR  
 RP SEQUENCE 1023 AA; 119521 MW; DQACFF6A0A5D0A1 CRG64;  
 Best Local Similarity 34.2%; Score 115; DB 4; Length 1023;  
 Matches 19; Conservative 6; Mismatches 28; Indels 0; Gaps 0;  
 OY 1 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
 DB 933 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55

ENEM; AB013059; BA06547.1; -.  
 DR InterPro; IPR001110; 19-like.  
 DR Pfam; PF00090; tps1; 6.  
 DR SMART; SM0209; TSP1; 7.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS0092; TSP1; 5.  
 KM Repeat: signal; 1 26  
 FT SIGNAL  
 FT CHAIN 27 766  
 FT ADAM-TSL2  
 FT DOMAIN 1 422  
 FT TSP TYPE-1  
 FT DOMAIN 422 474  
 FT TSP TYPE-1  
 FT DOMAIN 482 538  
 FT TSP TYPE-1  
 FT DOMAIN 568 625  
 FT TSP TYPE-1  
 FT DOMAIN 625 759  
 FT TSP TYPE-1  
 FT NON\_TIR  
 RP SEQUENCE 766 AA; 85997 MW; A42613B74E91719 CRG64;  
 Query Match 32.4%; Score 114; DB 4; Length 766;  
 Best Local Similarity 44.0%; Pred. No. 6.1e-06;  
 Matches 22; Conservative 7; Mismatches 19; Indels 2; Gaps 2;  
 OY 1 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 50  
 DB 707 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 50  
 RESULT 14  
 ID Q95428 PRELIMINARY; PRT: 1235 AA.  
 AC Q95428,  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID:9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 EX MEDLINE:14031619; PubMed:10571462; Hiroawa M, Nomura N, Ohara O,  
 RT "Prediction of the coding sequences of unidentified human genes. XV.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins." J Biol Chem 269:14515-14519, 1994.  
 DR ENEM; AB013059; BA06547.1; -.  
 DR InterPro; IPR001110; 19-like.  
 DR InterPro; IPR002884; 19-like.  
 DR Pfam; PF00647; 45; 3. 19-like.  
 DR Pfam; PF00090; tps1; 6.  
 DR SMART; SM0209; TSP1; 4.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS0092; TSP1; 6.  
 DR NON\_TIR  
 RP SEQUENCE 1235 AA; 133477 MW; A0844CC43F9B350 CRG64;  
 Query Match 32.4%; Score 114; DB 4; Length 1235;  
 Best Local Similarity 44.0%; Pred. No. 9.8e-06;  
 Matches 26; Conservative 3; Mismatches 21; Indels 6; Gaps 3;  
 OY 1 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55  
 DB 933 MWUWMECSVGGDQIGRRTCT-LQPQAQVADFCQHLKPVTVRGCC 55



GenCore version 5.1.6

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OW protein - protein search, using sw model

Run on: March 13, 2004, 07:28:59 ; Search time 1.48854 Seconds

Title: US-09-836-712-2\_COPY\_1099\_1156

Sequence: 1 MVTGMEWCSGDIQRR.....QHLPEVTVGCMAGPQQ 58

Scoring table: BLOSUM62 Gap: 10.0, Gapext: 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: Geneseq\_29Jan04.\*

2: Geneseq\_19804.\*

3: Geneseq\_20000.\*

4: Geneseq\_2018.\*

5: Geneseq\_2028.\*

6: Geneseq\_2030.\*

7: Geneseq\_2031.\*

8: Geneseq\_2034.\*

Read No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	346	100.0	1297 6	Aac16618 Human von
2	346	100.0	1327 6	Aac16620 Human von
3	346	100.0	1353 6	Aae24449 Human von
4	346	100.0	1354 6	Aae24450 Human von
5	346	100.0	1378 6	Aac16619 Human von
6	346	100.0	1416 5	Abb04153 Human ADA
7	346	100.0	1427 5	Aae24450 Human von
8	346	100.0	1427 5	Aae24450 Human von
9	346	100.0	1445 5	Abb9325 Human PMW
10	122.5	35.4	237 5	Abb05011 Human can
11	122.5	35.4	237 5	Abb05011 Human can
12	122.5	35.4	398 7	Ade09552 Novel pro
13	122.5	35.4	407 7	Ade09552 Novel pro
14	122.5	35.4	372 7	Adc22076 Human pro
15	122.5	35.4	421 4	Aae05936 ADAM prot
16	122.5	35.4	451 6	Abb05026 Human nov
17	122.5	35.4	451 6	Abb05026 Human nov
18	122.5	35.4	645 4	Abb10454 Human cdl
19	122.5	35.4	645 4	Abb07041 Human cdl
20	122.5	35.4	707 7	Ade09579 Novel pro
21	122.5	35.4	707 7	Ade09579 Novel pro
22	122.5	35.4	1088 7	Aac30823 Human cel
23	122.5	35.1	367 8	Abb082162 Human NOV
24	121.5	35.1	367 8	Abb082162 Human NOV
25	121.5	35.1	373 4	Aae09595 Human gen
26	121.5	35.1	369 4	Aae09596 Human gen

ALIGNMENTS

RESULT 1	
Aac16618	Aac16618 standard; protein, 1297 aa.
XX	XX
AC	AAc16618;
XX	XX
XX	XX 15-MAY-2003 (first entry)
DE	DE Human Von Willebrand factor (VWF)-cleaving enzyme-related protein #5.
EE	EE Human, protease inhibitor; gene therapy, vWF-cleaving enzyme.
XX	XX von Willebrand factor-cleaving enzyme, thrombocytopenic purpura;
XX	XX myocardial infarction; cerebral infarction; arteriosclerosis;
XX	XX platelet thrombosis; stenosis.
GS	GS Homo sapiens.
FX	FX MO20028366-A1.
XX	XX
XX	XX 07-NOV-2002.
XX	XX
XX	XX 25-APR-2002; 2002MO-JP004141.
PR	PR 25-APR-2001; 2001JP-00128342.
PR	PR 27-JUL-2001; 2001JP-00227510.
PR	PR 28-SEP-2001; 2001JP-00323977.
XX	XX 25-JAN-2002; 2002JP-00017596.
PA	PA (KAGA) CHMO-SERO-THERAPEUTIC RES INST.
XX	XX
XX	XX Soejima K, Mizura N, Maeda H, Nozaki K, Hamamoto T, Nakagaki T;
XX	XX WFI; 2003-120479/11.
XX	XX
XX	XX N-FCDB; ARI21584.
XX	XX
XX	XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and
XX	XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for
XX	XX developing drugs for e.g. myocardial infarction and cerebral infarction.
XX	XX
XX	XX Claim 4; Page 92-101; 144pp; Japanese.
XX	XX
XX	XX This invention comprises the amino acid and coding sequence of a von
XX	XX Willebrand factor-cleaving enzyme. The amino acid sequence of
XX	XX the invention are useful in the diagnosis and treatment of
XX	XX thrombotic thrombocytopenic purpura, and in developing drugs for myocardial
XX	XX infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,
XX	XX stenosis, and platelet thrombosis. The invention also comprises a human von
XX	XX Willebrand factor (VWF)-cleaving enzyme-related protein



```

XX SQ Sequence 1297 AA;
XX Query Match 100.0%; Score 346; DB 6; Length 1297;
XX Best Local Similarity 100.0%; Pred. No. 4,1e-32;
XX Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 58
DB 1002 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 1059
RESULT 2
ID AAO16620 standard; protein; 1323 AA.
XX AC AAO16620;
XX SC Homo sapiens.
XX PR 07-NOV-2002.
XX DT 15-MAY-2003 (first entry)
XX XX
XX XX Human von Willebrand factor (vWF)-cleaving enzyme-related protein #7.
XX XX Human; protease inhibitor; gene therapy; vWF-cleaving enzyme;
XX XX von Willebrand factor-cleaving enzyme; thrombocytogenic purpura;
XX XX myocardial infarction; cerebral infarction; arteriosclerosis;
XX XX platelet thrombosis; stenosis.
XX XX
XX CS Homo sapiens.
XX PR 07-NOV-2002.
XX DT 07-NOV-2002.
XX XX
XX XX W0300289366.h1.
XX PR 25-APR-2002; 2002NO-JP004141.
XX DT 25-APR-2002.
XX XX
XX XX 25-APR-2001; 2002JP-00128242.
XX PR 28-SEP-2001; 2002JP-0032977.
XX DT 25-JAN-2002; 2002JP-0017594.
XX XX
XX XX (KAGA) CHEMO-SERO-THESAPRUTIC RES INST.
XX XX
XX XX Soejima K, Mimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;
XX XX WPI; 2003-120479/11.
XX DT N-PSDB; ABT12586.
XX XX
XX XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and
XX XX developing drugs for e.g. myocardial infarction and cerebral infarction.
XX XX
XX XX Claim 4; Page 112-121; 144pp; Japanese.
XX XX
XX XX The invention comprises the amino acid and coding sequence of a von
XX XX Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of
XX XX the invention are useful in the diagnosis and treatment of cerebral
XX XX infarction, cerebral infarction, arteriosclerosis, platelet thrombosis,
XX XX and stenosis. The present amino acid sequence represents a human von
XX XX Willebrand factor (vWF)-cleaving enzyme-related protein.
XX XX
XX XX Sequence 1353 AA;
XX SQ
XX Query Match 100.0%; Score 346; DB 5; Length 1353;
XX Best Local Similarity 100.0%; Pred. No. 4,1e-32;
XX Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 58
DB 1002 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 1059
RESULT 4
ID AAO16617 standard; protein; 1353 AA.
XX AC AAO16617;
XX SC Homo sapiens.
XX PR 20-NOV-2001; 2001NO-EP0013391.
XX DT 22-NOV-2000; 2000HS-00071224.
XX PR 11-APR-2001; 2001US-0083938.
XX DT 30-MAY-2002.
XX XX
XX XX W0300242441-A2.
XX PR 20-NOV-2001; 2001NO-EP0013391.
XX DT 22-NOV-2000; 2000HS-00071224.
XX PR 11-APR-2001; 2001US-0083938.
XX DT 30-MAY-2002.
XX XX
XX XX (BAXT) BAXTER AG.
XX XX
XX XX Lammle B, Gerritsen HE, Furlan M, Turecek P, Schwarz H;
XX XX Schefflinger F, Antoine G, Kerschbaumer R, Tagliavacca L;
XX XX Zimmermann K, Voelkel D;
XX XX WPI; 2002-479950/31.
XX XX
XX XX Novel isolated or substantially purified von Willebrand factor-cleaving
XX XX protease, useful for producing preparations for therapy of thrombosis and
XX XX thromboembolic disease such as thrombotic thrombocytopenic purpura.
XX XX
XX XX Claim 1; Page 64-68; 99pp; English.
XX XX
XX XX The invention relates to an isolated or substantially pure von Willebrand
XX XX factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for
XX XX purifying vWF which involves providing vWF-cp as a ligand, contacting a
XX XX solution containing vWF with the ligand and recovering from the ligand purified
XX XX vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies
XX XX which involves immunising an animal with vWF-cp and isolating the anti-
XX XX body. The invention also relates to a method for the treatment of thrombotic
XX XX thromboembolic disease such as thrombotic thrombocytopenic purpura (TTP),
XX XX Henoch-Schönlein purpura, pre-eclampsia, neonatal thrombocytopenia or
XX XX platelet thrombosis. The invention also relates to a method for the
XX XX plasmatic or recombinantly produced vWF. The invention is useful for
XX XX construction expression systems and generating transgenic animals which
XX XX express the polypeptide in vivo. The present sequence is human vWF-cp
XX XX fragment.
XX XX
XX XX Sequence 1353 AA;
XX SQ
XX Query Match 100.0%; Score 346; DB 5; Length 1353;
XX Best Local Similarity 100.0%; Pred. No. 4,1e-32;
XX Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 58
DB 1002 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 1059
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ID AAO16617 standard; protein; 1353 AA.
XX AC AAO16617;
XX SC Homo sapiens.
XX PR 20-NOV-2001; 2001NO-EP0013391.
XX DT 22-NOV-2000; 2000HS-00071224.
XX PR 11-APR-2001; 2001US-0083938.
XX DT 30-MAY-2002.
XX XX
XX XX W0300242441-A2.
XX PR 20-NOV-2001; 2001NO-EP0013391.
XX DT 22-NOV-2000; 2000HS-00071224.
XX PR 11-APR-2001; 2001US-0083938.
XX DT 30-MAY-2002.
XX XX
XX XX (BAXT) BAXTER AG.
XX XX
XX XX Lammle B, Gerritsen HE, Furlan M, Turecek P, Schwarz H;
XX XX Schefflinger F, Antoine G, Kerschbaumer R, Tagliavacca L;
XX XX Zimmermann K, Voelkel D;
XX XX WPI; 2002-479950/31.
XX XX
XX XX Novel isolated or substantially purified von Willebrand factor-cleaving
XX XX protease, useful for producing preparations for therapy of thrombosis and
XX XX thromboembolic disease such as thrombotic thrombocytopenic purpura.
XX XX
XX XX Claim 1; Page 64-68; 99pp; English.
XX XX
XX XX The invention relates to an isolated or substantially pure von Willebrand
XX XX factor-cleaving protease (vWF-cp) polypeptide. vWF-cp is useful for
XX XX purifying vWF which involves providing vWF-cp as a ligand, contacting a
XX XX solution containing vWF with the ligand and recovering from the ligand purified
XX XX vWF. vWF-cp is useful for producing anti-vWF cp polypeptide antibodies
XX XX which involves immunising an animal with vWF-cp and isolating the anti-
XX XX body. The invention also relates to a method for the treatment of thrombotic
XX XX thromboembolic disease such as thrombotic thrombocytopenic purpura (TTP),
XX XX Henoch-Schönlein purpura, pre-eclampsia, neonatal thrombocytopenia or
XX XX platelet thrombosis. The invention also relates to a method for the
XX XX plasmatic or recombinantly produced vWF. The invention is useful for
XX XX construction expression systems and generating transgenic animals which
XX XX express the polypeptide in vivo. The present sequence is human vWF-cp
XX XX fragment.
XX XX
XX XX Sequence 1353 AA;
XX SQ
XX Query Match 100.0%; Score 346; DB 5; Length 1323;
XX Best Local Similarity 100.0%; Pred. No. 4,1e-32;
XX Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 58
DB 1027 NHVWTWMECSVSGDGIQRERTCLGFOQAQPVPAFQCHLKPFTVTCAGAGCTGG 1084
RESULT 3

```

15-MAY-2003 (first entry)  
 DE Human von Willebrand factor (vWF)-cleaving enzyme-related protein #4.  
 KW Human, protease inhibitor; gene therapy; vWF-cleaving enzyme;  
 KW von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 OS Homo sapiens.  
 XX W0200289366-A1.  
 XX 07-NOV-2002.  
 XX 25-APR-2002; 2002MO-JP004141.  
 XX 25-APR-2001; 2001JP-00128342.  
 XX 27-JUL-2001; 2001JP-00227510.  
 XX 28-SEP-2001; 2001JP-00032977.  
 XX 25-JAN-2002; 2002JP-00017596.  
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
 XX Soejima K, Nimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;  
 XX WFI; 2003-120479/11.  
 XX N-PSDB; AB12355.  
 XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
 XX developing drugs for e.g. myocardial infarction and cerebral infarction.  
 XX Claim 4; Page 102-111; 144pp; Japanese.  
 XX The invention comprises the amino acid and coding sequence of a von  
 XX Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 XX the invention are useful in the diagnosis and treatment of  
 XX thrombocytopenic purpura, and in developing drugs for myocardial  
 XX infarction, cerebral infarction, platelet thrombosis, arteriosclerosis,  
 XX and stenosis. The present amino acid sequence represents a human von  
 XX Willebrand factor (vWF)-cleaving enzyme-related protein  
 XX Sequence 1378 AA;  
 XX Query Match 100.0%; Score 346; DB 6; Length 1378;  
 XX Best Local Similarity 100.0%; Pred. No. 4, 2e-32;  
 XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX 1 HNGVWMECSGCGTQRRRTCTCLGQAQAPVADPQQLKFTVTRGCMAGPCVQ 58  
 XX 1027 HNGVWMECSGCGTQRRRTCTCLGQAQAPVADPQQLKFTVTRGCMAGPCVQ 1084  
 XX RESULT 6  
 XX DBS 13  
 XX ID A8B04153 standard; protein; 1416 AA.  
 XX A8B04153  
 XX 26-MAY-2002 (first entry)  
 XX Human ADAMTS-M polypeptide.  
 XX Osteoarthritis; rheumatoid arthritis; inflammatory bowel disease;  
 XX Crohn's disease; asthma; Alzheimer's disease; organ transplant rejection;  
 XX cachexia; allergy; cancer; leukemia; lymphoma; osteoporosis;  
 XX osteoarthritis; osteoporosis; osteoporosis; osteoporosis; stroke;  
 XX neurodegenerative disease; autoimmune disorder; Huntington's;  
 XX Parkinson's; migraine; pain; depression; multiple sclerosis; burn;  
 XX infertility; diabetic shock; gene therapy; ADAMTS-M;  
 XX A Disintegrin And Metalloprotease; thrombospondin domain.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Key 1..37  
 XX Peptide /label: Prodomain  
 XX /note: The mature form of the ADAMTS-M protein is  
 XX /note: released by autocatalytic cleavage of the prodomain.  
 XX /label: Cleavage-site  
 XX /label: Furin\_Cleavage\_site  
 XX Protein /label: Mature ADAMTS-M protein  
 XX /label: Mature ADAMTS-M protein  
 XX /note: The mature form of the ADAMTS-M protein is

15-MAY-2003 (first entry)  
 DE Human von Willebrand factor (vWF)-cleaving enzyme-related protein #4.  
 KW Human, protease inhibitor; gene therapy; vWF-cleaving enzyme;  
 KW von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 OS Homo sapiens.  
 XX W0200289366-A1.  
 XX 07-NOV-2002.  
 XX 25-APR-2002; 2002MO-JP004141.  
 XX 25-APR-2001; 2001JP-00128342.  
 XX 27-JUL-2001; 2001JP-00227510.  
 XX 28-SEP-2001; 2001JP-00032977.  
 XX 25-JAN-2002; 2002JP-00017596.  
 XX (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
 XX Soejima K, Nimura N, Maeda H, Nozaki C, Hamamoto T, Nakagaki T;  
 XX WFI; 2003-120479/11.  
 XX N-PSDB; AB12355.  
 XX von Willebrand factor-cleaving enzyme, applicable in diagnosis of, and  
 XX supplementary therapy for, thrombotic thrombocytopenic purpura, and for  
 XX developing drugs for e.g. myocardial infarction and cerebral infarction.  
 XX Claim 4; Page 82-92; 144pp; Japanese.  
 XX The invention comprises the amino acid and coding sequence of a von  
 XX Willebrand factor (vWF)-cleaving enzyme. The DNA and protein sequences of  
 XX the invention are useful in the diagnosis and treatment of  
 XX thrombocytopenic purpura, and in developing drugs for myocardial  
 XX infarction, cerebral infarction, platelet thrombosis, arteriosclerosis,  
 XX and stenosis. The present amino acid sequence represents a human von  
 XX Willebrand factor (vWF)-cleaving enzyme-related protein  
 XX Sequence 1353 AA;  
 XX Query Match 100.0%; Score 346; DB 6; Length 1353;  
 XX Best Local Similarity 100.0%; Pred. No. 4, 2e-32;  
 XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX 1 HNGVWMECSGCGTQRRRTCTCLGQAQAPVADPQQLKFTVTRGCMAGPCVQ 58  
 XX 1002 HNGVWMECSGCGTQRRRTCTCLGQAQAPVADPQQLKFTVTRGCMAGPCVQ 1059  
 XX RESULT 5  
 XX DBS 13  
 XX ID A0016619 standard; protein; 1378 AA.  
 XX A0016619  
 XX 15-MAY-2003 (first entry)  
 XX Human von Willebrand factor (vWF)-cleaving enzyme-related protein #6.  
 KW Human, protease inhibitor; gene therapy; vWF-cleaving enzyme;  
 KW von Willebrand factor-cleaving enzyme; thrombocytopenic purpura;  
 KW myocardial infarction; cerebral infarction; arteriosclerosis;  
 KW platelet thrombosis; stenosis.  
 OS Homo sapiens.  
 XX W0200289366-A1.







Query Match 35.4%; Score 122.5; DB 7; Length 358;  
 Best Local Similarity 41.0%; Pred. No. 3,6e-06;  
 Matches 29; Conservative 7; Mismatches 20; Indels 9; Gaps 3;  
 Cy 1 WNVITWELSSGDIQRDRTCC--LIPQADAPVADICMLPKVTVAGCGAPGVG 57  
 DQ 180 WITPWEELSSGSGTIRDIIVSLKLTETVTSVSN\_CSHLPPAPLQ-----PQD 233  
 Oy 58 Q 58  
 DQ 234 Q 234  
 RESULT 12  
 AED05698  
 ID AAE09598 standard; protein; 372 AA.  
 XX AC  
 XX CC  
 XX DT 22-NOV-2001 (first entry)  
 XX XZ Human gene 9 encoding novel protein HUCW06, SEQ ID NO:45.  
 XX XZ Human, cytosolic; gene therapy; inflammatory disorder; neural disorder;  
 KW Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;  
 KW Parkinson's disease; Alzheimer's disease; immune system disorder; AIDS;  
 KW reproductive disorder; Crohn's disease; pulmonary disorder; cancer;  
 KW myocardial infarction; glomerulonephritis; nephrotic syndrome; tumour;  
 KW haematopoietic disorder; thimble; asthma; diabetes; atherosclerosis;  
 KW anti-sense therapy; endocrine disorder; leishmaniasis.  
 CS Homo Sapiens.  
 XX AC  
 XX CC  
 XX DT 02-AUG-2001.  
 XX XZ WC2001155202-A1.  
 XX XZ 17-JAN-2001; 2001NC-U8601125.  
 XX 31-JAN-2000; 2000US-0178065P.  
 XX 24-FEB-2000; 2000US-0185664P.  
 XX 16-MAR-2000; 2000US-0186350P.  
 XX 16-MAR-2000; 2000US-0189874P.  
 XX 18-APR-2000; 2000US-0190123P.  
 XX 19-MAY-2000; 2000US-0205515P.  
 XX 07-JUN-2000; 2000US-0209467P.  
 XX 30-JUN-2000; 2000US-0213155P.  
 XX 07-JUL-2000; 2000US-0216647P.  
 XX 07-JUL-2000; 2000US-0216805P.  
 XX 11-JUL-2000; 2000US-0217496P.  
 XX 14-JUL-2000; 2000US-0218240P.  
 XX 26-JUL-2000; 2000US-0219638P.  
 XX 14-AUG-2000; 2000US-0225139P.  
 XX 14-AUG-2000; 2000US-0225198P.  
 XX 14-AUG-2000; 2000US-0225479P.  
 XX 14-AUG-2000; 2000US-0225669P.  
 XX 14-AUG-2000; 2000US-0225672P.  
 XX 14-AUG-2000; 2000US-0225895P.  
 XX 14-AUG-2000; 2000US-0225447P.  
 XX 14-AUG-2000; 2000US-0225757P.  
 XX 14-AUG-2000; 2000US-0227589P.  
 XX 18-AUG-2000; 2000US-0232759P.  
 XX 22-AUG-2000; 2000US-0236681P.  
 XX 22-AUG-2000; 2000US-0236689P.  
 XX 22-AUG-2000; 2000US-0237162P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 01-SEP-2000; 2000US-0228077P.  
 PR 01-SEP-2000; 2000US-0228343P.  
 PR 01-SEP-2000; 2000US-0229133P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229348P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230477P.  
 PR 08-SEP-2000; 2000US-0231143P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231433P.  
 PR 08-SEP-2000; 2000US-0231443P.  
 PR 08-SEP-2000; 2000US-0231448P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 12-SEP-2000; 2000US-0231958P.  
 PR 12-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234231P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 21-SEP-2000; 2000US-0234988P.  
 PR 25-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235534P.  
 PR 28-SEP-2000; 2000US-0235627P.  
 PR 28-SEP-2000; 2000US-0235658P.  
 PR 28-SEP-2000; 2000US-0235676P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237042P.  
 PR 11-OCT-2000; 2000US-0239393P.  
 PR 11-OCT-2000; 2000US-0239393P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241285P.  
 PR 20-OCT-2000; 2000US-0241789P.  
 PR 20-OCT-2000; 2000US-0241789P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 01-NOV-2000; 2000US-0244674P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246521P.  
 PR 08-NOV-2000; 2000US-0246521P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246533P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246626P.  
 PR 08-NOV-2000; 2000US-0246626P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-043210P.  
 PR 17-NOV-2000; 2000US-043211P.  
 PR 17-NOV-2000; 2000US-043212P.  
 PR 17-NOV-2000; 2000US-043213P.  
 PR 17-NOV-2000; 2000US-043214P.  
 PR 17-NOV-2000; 2000US-043215P.  
 PR 17-NOV-2000; 2000US-043216P.  
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 PR 17-NOV-2000; 2000US-043219P.  
 PR 17-NOV-2000; 2000US-043220P.  
 PR 17-NOV-2000; 2000US-043221P.  
 PR 17-NOV-2000; 2000US-043222P.  
 PR 17-NOV-2000; 2000US-043223P.  
 PR 17-NOV-2000; 2000US-043224P.  
 PR 17-NOV-2000; 2000US-043225P.  
 PR 17-NOV-2000; 2000US-043226P.  
 PR 17-NOV-2000; 2000US-043227P.  
 PR 17-NOV-2000; 2000US-043228P.  
 PR 17-NOV-2000; 2000US-043229P.  
 PR 17-NOV-2000; 2000US-043230P.  
 PR 01-DEC-2000; 2000US-050310P.  
 PR 03-DEC-2000; 2000US-050310P.  
 PR 03-DEC-2000; 2000US-050310P.  
 PR 06-DEC-2000; 2000US-051479P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 08-DEC-2000; 2000US-051846P.  
 PR 11-DEC-2000; 2000US-051909P.  
 PR 11-DEC-2000; 2000US-052405P.  
 PR 11-DEC-2000; 2000US-052405P.  
 PR 03-JAN-2001; 2000US-052676P.  
 PR (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Barash BC, Ruben SM.  
 XX WPI; 2001-451925/4B.  
 XX N-PSDB; Adu16756.  
 XX Isolated polypeptide for treating, preventing and/or proposing medical  
 XX disorders and also for testing and detection e.g. diagnosis and screening  
 XX for agonists.  
 XX Claim 1; SEQ ID NO 45; 463pp; English.  
 XX Adu16750-Adu16775 represent cDNAs corresponding to novel human protein  
 XX "Adu16750-Adu16759; Adu16775 represent the proteins they encode. Adu16777  
 XX and their DNAs are useful for diagnosing, treating, preventing and/or  
 XX screening for various diseases, including Alzheimer's disease, Parkinson's  
 XX disease (e.g. Parkinson's disease, Alzheimer's disease), immune system  
 XX disorders, autoimmune diseases (e.g., rheumatoid arthritis),  
 XX muscular disorders, reproductive disorders, gastrointestinal disorders  
 XX (e.g., Crohn's disease, ulcerative colitis), endocrine disorders, renal  
 XX disorders (glomerulonephritis, nephrotic syndrome), cancerous  
 XX diseases and conditions (breast cancer), hyperproliferative disorders  
 XX (e.g., hematopoietic disorders, respiratory disorders (rhinitis, asthma),  
 XX angiogenic disorders, diabetes, atherosclerosis, endocrine disorders,  
 XX pregnancy-related disorders and infections. The novel protein may also be  
 XX used to aid wound healing and epithelial cell proliferation, to prevent  
 XX skin aging due to sunburn, to maintain organs before transplantation, for  
 XX supporting cell culture of primary tissues, to regenerate tissues, to  
 XX improve the health of aged individuals, to improve the health of diseased  
 XX individuals, and can be used as a food additive or preservative to modify storage  
 XX properties. The present sequence represents a novel human protein of the  
 XX invention. Note: the sequence data for this patent did not form part of  
 XX the prior art. (filed in US Patent Office). The sequence data was submitted  
 XX from WPI at [ftp.wpi.int/pub/published\\_pat\\_sequences](http://ftp.wpi.int/pub/published_pat_sequences)  
 XX Query Match: 35.4%; Score: 122.5; Db: 4; Length: 372;  
 XX Matches: 25; Conservative: 7; Mismatches: 20; Indels: 9; Gaps: 3;

QY 1 WNWGHWGCVSGDQIGRRDTC---LQDQAQVADPQCHLQFVETVRCWACRQV 57  
 DB 212 WTGPGWGCSSGSGGRRDITCVICSGTGNWTSFSL-LSHLPFPAAG-----RQD 265  
 QY 58 Q 58  
 DB 266 Q 266  
 RESULT 13  
 ID NC22076 standard; protein; 372 AA.  
 AC AC22076;  
 XX 18-DEC-2003 (first entry)  
 XX Human protein from secreted protein gene 9 #1.  
 XX Secreted protein; cytosolic; antibacterial; virulence; neuroprotective;  
 XX gynaecological; gastrointestinal; Gen; cardiac; cardiovascular; Gen;  
 XX nephrologic; antihemorrhagic; muscular; muscular; muscular; Gen;  
 XX antiallergic; cancer; bacterial infection; viral infection;  
 XX neural disorder; immune system disorder; blood disorder;  
 XX muscular disorder; reproductive disorder; endocrine disorder;  
 XX inflammatory disorder; proliferative disorder; Human.  
 XX Homo sapiens.  
 XX US2003052681-A1.  
 XX 01-MAY-2003.  
 XX 07-MAY-2002; 2002US-00091391.  
 XX 11-MAY-2000; 2000US-017865P.  
 XX 04-FEB-2000; 2000US-018028P.  
 XX 04-FEB-2000; 2000US-018466P.  
 XX 02-MAR-2000; 2000US-018635P.  
 XX 11-MAR-2000; 2000US-019007P.  
 XX 16-APR-2000; 2000US-0198123P.  
 XX 19-MAY-2000; 2000US-0205513P.  
 XX 26-JUN-2000; 2000US-021486P.  
 XX 30-JUN-2000; 2000US-0215133P.  
 XX 07-JUL-2000; 2000US-021664P.  
 XX 11-JUL-2000; 2000US-021789P.  
 XX 11-JUL-2000; 2000US-021796P.  
 XX 14-JUL-2000; 2000US-021820P.  
 XX 26-JUL-2000; 2000US-022064P.  
 XX 14-AUG-2000; 2000US-024518P.  
 XX 14-AUG-2000; 2000US-025137P.  
 XX 14-AUG-2000; 2000US-025266P.  
 XX 14-AUG-2000; 2000US-025270P.  
 XX 14-AUG-2000; 2000US-025447P.  
 XX 14-AUG-2000; 2000US-025457P.  
 XX 14-AUG-2000; 2000US-025758P.  
 XX 18-AUG-2000; 2000US-025759P.  
 XX 18-AUG-2000; 2000US-026279P.  
 XX 22-AUG-2000; 2000US-026868P.  
 XX 22-AUG-2000; 2000US-027182P.  
 XX 23-AUG-2000; 2000US-027009P.







CX	protein
XX	Sequence 491 AA:
QQ	Score 122.5; CB 6; Length 491;
SQ	Query Varch
	Best Local Similarity 41.0%; Pred No. 5a-06;
SS	Matches 25; Conservative 7; Mismatches 20; Indels 9; Gaps 3
QY	1 MWKTHMCEVCGDGTGSRDFC---LGRCAAPVPANFCCLIKETVTUHCACPGC 57
DY	
DB	331 WYTGNGECSGSGSCGLDLCVSLGTEFTSTSN-CSHLRPPLAQ-----PDG 384
Dc	58 Q 58
Dd	385 O 385

Search completed: March 13, 2004, 07:39:07  
Job time : 9.48854 sec





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; LENGTH: 491
; REGION: 1-491
; ORGANISM: Homo sapiens
US-10-125-470-10

Query Match      35.4%; Score 122.5; DB 13; Length 491;
Best Local Similarity 41.0%; Pred. No. 1.1e-05;
Matches 25; Conservative 7; Mismatches 20; Indels 9; Gaps 3;

Oy 1 WHVTVWGVSVSGDGIQRDRDTCLGPA--LGPQAQVPADECHLPKPVTVGCGNAGPVG 57
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Oy 58 Q 58
DB 385 Q 385

RESULT 7
US-10-125-452-10
; Application US/0125452
; Publication No. US20020173641
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; FILE REFERENCE: P176622
; CURRENT APPLICATION NUMBER: US/10/125.452
; CURRENT FILING DATE: 2002-04-19
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 09/112.907
; PRIOR FILING DATE: 2000-11-16
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/178.717
; PRIOR FILING DATE: 2000-01-28
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/136.388
; PRIOR FILING DATE: 1999-05-27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
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; REGION: 1-491
; ORGANISM: Homo sapiens
US-10-125-452-10

Query Match      35.4%; Score 122.5; DB 13; Length 491;
Best Local Similarity 41.0%; Pred. No. 1.1e-05;
Matches 25; Conservative 7; Mismatches 20; Indels 9; Gaps 3;

Oy 1 WHVTVWGVSVSGDGIQRDRDTCLGPA--LGPQAQVPADECHLPKPVTVGCGNAGPVG 57
DB 331: WYGPVNGEISCSGSGTQRDIICVSKLGTGFVTSSEN-CHLPFPFPAQ-----PQCG 384
Oy 58 Q 58
DB 385 Q 385

RESULT 8
US-09-764-853-762
; Application US/0974853
; Publication No. US2002030967A1
; GENERAL INFORMATION:
; APPLICANT: Roen et al.
; FILE REFERENCE: N2002030967A1
; CURRENT APPLICATION NUMBER: US/09/764.853
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 519

; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 519
; REGION: 1-519
; ORGANISM: Homo sapiens
US-09-764-853-762

Query Match      35.1%; Score 121.5; DB 14; Length 56;
Best Local Similarity 47.9%; Pred. No. 1.4e-02;
Matches 24; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

Oy 1 WHVTVWGVSVSGDGIQRDRDTCLGPAQVPADECHLPKPVTVGCGNAGPVG 55
DB 3 NGLZPWSQSTGVRGKLLCGAANT-LPESQTSLPFPELCYVLCGC 56
Oy 10
US-10-087-887-16

; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 56
; REGION: 1-56
; ORGANISM: Homo sapiens
US-10-087-887-16

Query Match      35.1%; Score 121.5; DB 14; Length 56;
Best Local Similarity 47.9%; Pred. No. 1.4e-02;
Matches 24; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

Oy 1 WHVTVWGVSVSGDGIQRDRDTCLGPAQVPADECHLPKPVTVGCGNAGPVG 55
DB 3 NGLZPWSQSTGVRGKLLCGAANT-LPESQTSLPFPELCYVLCGC 56
Oy 10
US-10-087-887-16

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> Sequence 15, Application US/10087897
> GENERAL INFORMATION:
> Patent No. US20020196957A1
> APPLICANT: Kekuda, Ramesh
> APPLICANT: Conley, Pamela B.
> APPLICANT: Hart, Matthew
> APPLICANT: Tomlinson, James E.
> APPLICANT: Popper, James N.
> APPLICANT: Leach, Martin D.
> APPLICANT: Zethusen, Bryan D.
> APPLICANT: Komuves, Laszlo
> APPLICANT: Kishimoto, Akihiro
> TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
> FILE REFERENCE: 21402-285
> CURRENT FILING DATE: 2001-03-01
> PRIOR FILING DATE: 2001-03-01
> PRIOR APPLICATION NUMBER: 60/273,049
> PRIOR FILING DATE: 2001-03-02
> PRIOR FILING DATE: 2001-03-09
> PRIOR FILING DATE: 2001-03-09
> PRIOR APPLICATION NUMBER: 60/277,791
> PRIOR FILING DATE: 2001-03-21
> PRIOR FILING DATE: 2001-04-01
> PRIOR FILING DATE: 2001-04-03
> PRIOR FILING DATE: 2001-04-03
> PRIOR FILING DATE: 2001-04-10
> PRIOR FILING DATE: 2001-04-10
> PRIOR APPLICATION NUMBER: 60/282,537
> PRIOR APPLICATION NUMBER: 60/282,867
> PRIOR FILING DATE: 2001-04-10
> PRIOR FILING DATE: 2001-04-10
> SOFTWARE: Outadsequist version 0.1
> SEQ ID NO : 6
> LENGTH: 283
> ORGANISM: Homo sapiens
> TYPE: PRT
> US-10-087-887-56

Query Match
Best Local Similarity 35.1%; Score 121.5; DB 14; Length 283;
Matches 21; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

OY 1 MHGTWMECVSGDGIQRSDTCLGPAQAQVADFCQHPVTVGQWAGPC 55
DB 57 NSLGPWQSQCNTCGVWKEMLLKGSAET-LFSSQTSJLPRPELQSGCVLGR 110

RESULT 11
US-09-764-903-46
> Sequence 16, Application US/0976903
> Patent No. US2002020967A1
> GENERAL INFORMATION:
> APPLICANT: Rosen et al.
> FILE REFERENCE: P7228
> CURRENT APPLICATION NUMBER: US/09/764,903
> CURRENT FILING DATE: 2001-01-17
> NUMBER OF SEQ ID NOS: 67
> SOFTWARE: PatentIn Ver. 2.0
> SEQ ID NO 46
> LENGTH: 367
> ORGANISM: Homo sapiens
> TYPE: PRT
> US-09-764-903-46

Query Match
Best Local Similarity 35.1%; Score 121.5; DB 9; Length 367;
Matches 21; Conservative 9; Mismatches 24; Indels 1; Gaps 1;

OY 1 MHGTWMECVSGDGIQRSDTCLGPAQAQVADFCQHPVTVGQWAGPC 55
DB 143 NSLGPWQSQCNTCGVWKEMLLKGSAET-LFSSQTSJLPRPELQSGCVLGR 196

RESULT 13
US-10-130-801-46
> Sequence 16, Application US/10120801
> Publication No. US20030203643A1
> APPLICANT: Pena, Carol
> APPLICANT: Guo, Xisao;ia
> APPLICANT: Shimwae, Richard
> APPLICANT: Kishimoto, Akihiro
> APPLICANT: Kekuda, Ramesh
> APPLICANT: Spytek, Kimberly
> APPLICANT: Mehrahan, Foad
> APPLICANT: Kishimoto, Akihiro
> APPLICANT: Malyankar, Uriel
> APPLICANT: Wasserman, Scott
> APPLICANT: Salinger, Shomrit
> APPLICANT: Kishimoto, Akihiro
> APPLICANT: Gunther, Erik
> APPLICANT: Komuves, Laszlo
> TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
> CURRENT APPLICATION NUMBER: US/10/130,801
> CURRENT FILING DATE: 2002-04-11
> PRIOR APPLICATION NUMBER: 60/285,746
> PRIOR APPLICATION NUMBER: 60/286,066
> PRIOR FILING DATE: 2001-04-24
> PRIOR FILING DATE: 2001-04-24
> PRIOR FILING DATE: 2001-04-24
> PRIOR FILING DATE: 2001-04-24
> PRIOR APPLICATION NUMBER: 60/288,334
> PRIOR FILING DATE: 2001-05-03
> PRIOR FILING DATE: 2001-05-03
> PRIOR FILING DATE: 2001-05-11
> PRIOR FILING DATE: 2001-05-11
> PRIOR APPLICATION NUMBER: 60/332,284

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PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/285609  
NUMBER OF SEQ ID NOS: 155  
SEQUENCE TYPE: Patent in Ver. 2.1  
SEQ ID NO 46  
LENGTH: 1081  
TYPE: PRT  
ORGANISM: Human  
US-10-120-801-46

Query Match 35.1%; Score 121.5; DB 15; Length 1081;  
Best Local Similarity 38.2%; Pred. No. 3.4e-05;  
Matches 21; Conservative 9; Mismatches 24; Indels 1; Gaps 1;  
Qy 1 HWYVWMECSVCGDIOGRDTCGLQQAQVPAFDCQHLKPKVTVRGWACPC 55  
Db 994 NSLWMSQSCGTCGRVRELLKGSAAH-LFSSQTSLEPRLQVLCVGRK 1047

RESULT 14  
US-10-120-801-45  
Sequence 45; Application US/10/20801  
Current Application No. US20030203843A1  
GENERAL INFORMATION  
APPLICANT: Pena, Carol  
APPLICANT: Guo, Xiaojia  
APPLICANT: Kishore, Richard  
APPLICANT: Padigara, Muralidhara  
APPLICANT: Keshu, Ramesh  
APPLICANT: Speyk, Kimberly  
APPLICANT: Chitrabhan, N  
APPLICANT: Mahankar, Urel  
APPLICANT: Maserman, Scott  
APPLICANT: Sridharan, G  
APPLICANT: Sulphon, Glenda  
APPLICANT: Gunther, Erik  
APPLICANT: Komuves, Laszlo  
APPLICANT: Vargha, Laszlo  
FILE REFERENCE: 21402-34105 and Nucleic Acids Encoding Same  
CURRENT APPLICATION NUMBER: US/10/120,801  
PRIOR FILING DATE: 2002-04-11  
PRIOR FILING DATE: 2001-04-23  
PRIOR FILING DATE: 2001-04-23  
PRIOR APPLICATION NUMBER: 60/285608  
PRIOR FILING DATE: 2001-04-24  
PRIOR FILING DATE: 2001-04-25  
PRIOR FILING DATE: 2001-04-25  
PRIOR APPLICATION NUMBER: 60/289334  
PRIOR FILING DATE: 2001-05-03  
PRIOR FILING DATE: 2001-05-03  
PRIOR APPLICATION NUMBER: 60/322284  
PRIOR FILING DATE: 2001-09-14  
PRIOR FILING DATE: 2001-09-14  
PRIOR FILING DATE: 2001-09-14  
PRIOR FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 155  
SOFTWARE: Patent in Ver. 2.1  
LENGTH: 1123  
TYPE: PRT  
ORGANISM: Human  
US-10-120-801-45

Query Match 35.1%; Score 121.5; DB 15; Length 1123;  
Best Local Similarity 38.2%; Pred. No. 3.4e-05;  
Matches 21; Conservative 9; Mismatches 24; Indels 1; Gaps 1;  
Qy 1 HWYVWMECSVCGDIOGRDTCGLQQAQVPAFDCQHLKPKVTVRGWACPC 55  
Db 861 NSLWMSQSCGTCGRVRELLKGSAAH-LFSSQTSLEPRLQVLCVGRK 114

RESULT 15  
US-10-161-493-124  
Sequence 124; Application US/10/61493  
Current Application No. US20030204855A1  
GENERAL INFORMATION  
APPLICANT: Anderson, David W  
APPLICANT: Zernhusen, Bryan D  
APPLICANT: Zhang, Wei  
APPLICANT: Ceman, Stacie J  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Gorman, Carol EA  
APPLICANT: Keshu, Ramesh  
APPLICANT: Speyk, Kimberly A  
APPLICANT: Leite, Mario W  
APPLICANT: Kestell, Lucia  
APPLICANT: Tausler Jr., Raymond J  
APPLICANT: Guo, Xiaojia Saaba  
APPLICANT: Miller, Shariene E  
APPLICANT: Hysat, Todd  
APPLICANT: Voss, Edward Z  
APPLICANT: Padigara, Muralidhara  
APPLICANT: Padigara, Muralidhara  
APPLICANT: Ji, Weizhen  
APPLICANT: Sridharan, G  
APPLICANT: Ediger, Shionet R  
APPLICANT: Millet, Isabelle  
APPLICANT: Ellemann, Karen  
APPLICANT: Vargha, Laszlo  
FILE REFERENCE: 21402-377A  
CURRENT APPLICATION NUMBER: US/10/161,493  
PRIOR FILING DATE: 2001-06-04  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/337,524  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,404  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,418  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,575  
PRIOR FILING DATE: 2001-06-07  
PRIOR APPLICATION NUMBER: 60/359,151  
PRIOR FILING DATE: 2001-06-11  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,573  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: 60/341,143  
PRIOR FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR APPLICATION NUMBER: 60/297,567  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 299  
SEQUENCE TYPE: PRT  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-161-493-124

Query Match 35.1%; Score 121.5; DB 15; Length 1162;  
Best Local Similarity 38.2%; Pred. No. 3.3e-05;  
Matches 21; Conservative 9; Mismatches 24; Indels 1; Gaps 1;  
Qy 1 HWYVWMECSVCGDIOGRDTCGLQQAQVPAFDCQHLKPKVTVRGWACPC 55

Db 536 WSLGWSCKTCDKQYNRELCKDASMT-IPSECTELPHRELSCVJDEC 989

Search completed: March 13, 2004, 08:07:06  
JCD time : 5.55567 secs





```

/ LENGTH: 1882
/ ORGANISM: Homo sapiens ADAMTS-9
/ FEATURES:
/ NAME/KEY: MOD_RES
/ OTHER INFORMATION: xaa = C
/ NAME/KEY: MOD_RES
/ LOCATION INFORMATION: xaa = Y
/ LOCATION INFORMATION: xaa = Y
US-09-369-364A-13

Query Match 34.4%; Score 115.5; DB 4; Length 1882;
Best Local Similarity 34.2%; Pred. No. 0.00015;
Matches 22; Conservative 6; Mismatches 24; Indels 1; Gaps 1;

QY 1 WNVWNGWVSVCDCGQRRRDTCLGPOAQAPVPADQFQHPKPVTVGWAQPC 55
|||||
DB 1392 WSTPMSGSCGSGHKNVYCKANG-SHLEEDYCHLAKHQRKRGRC 1445

RESULT 3
/ Sequence 8, Application US/0910491
/ Sequence 165, Application US/09800729
/ Sequence 165, Application US/09800729
/ GENERAL INFORMATION:
/ APPLICANT: Holtzman, Douglas A.
/ FILE REFERENCE: P204421
/ CURRENT FILING DATE: 1998-09-07
/ EARLIER FILING DATE: 1997-09-05
/ EARLIER APPLICATION NUMBER: US 60/054,961
/ EARLIER FILING DATE: 1997-09-06
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 481
/ TYPE: FAT
/ ORGANISM: Rattus rattus
US-09-130-491-8

Query Match 33.4%; Score 115.5; DB 4; Length 481;
Best Local Similarity 39.3%; Pred. No. 8.4e-06;
Matches 22; Conservative 6; Mismatches 25; Indels 3; Gaps 1;

QY 1 WNVWNGWVSVCDCGQRRRDTCLGPOAQAPVPADQFQHPKPVTVGWAQPC 56
|||||
DB 428 WVLGWSGCTSGSGWVRVRCDFSGQA---SDTCEALKFEDAPGSGPCL 480

RESULT 4
/ Sequence 8, Application US/0910491
/ Sequence 165, Application US/09800729
/ Sequence 165, Application US/09800729
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.; Human secreted proteins
/ FILE REFERENCE: P204421
/ CURRENT FILING DATE: 2001-01-08
/ EARLIER FILING DATE: 1998-09-07
/ EARLIER APPLICATION NUMBER: US 60/054,961
/ EARLIER FILING DATE: 1997-09-06
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ SEQ ID NO 155
/ LENGTH: 265
/ TYPE: FAT
/ ORGANISM: Homo sapiens

US-09-800-729-155

Query Match 32.4%; Score 112; DB 4; Length 2165;
Best Local Similarity 33.2%; Pred. No. 0.00015;
Matches 21; Conservative 6; Mismatches 26; Indels 2; Gaps 1;

QY 1 WNVWNGWVSVCDCGQRRRDTCLGPOAQAPVPADQFQHPKPVTVGWAQPC 55
|||||
DB 1371 WATGWTWACATGCGTQRRLLAC-RDWVRLPDEYCHLWKEVSTNCRDQC 1423

RESULT 5
/ Sequence 165, Application US/09800729
/ Sequence 165, Application US/09800729
/ Sequence 165, Application US/09800729
/ GENERAL INFORMATION:
/ APPLICANT: Ni et al.
/ FILE REFERENCE: P204421
/ CURRENT FILING DATE: US/09/800,729
/ CURRENT FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: PCT/US00/26013
/ PRIOR FILING DATE: 2000-09-22
/ PRIOR FILING DATE: 1999-09-24
/ NUMBER OF SEQ ID NOS: 217
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 55
/ LENGTH: 53
/ TYPE: FAT
/ ORGANISM: Homo sapiens
US-09-800-729-155

Query Match 31.1%; Score 107.5; DB 4; Length 53;
Best Local Similarity 42.6%; Pred. No. 7e-06; 19; Indels 5; Gaps 2;
Matches 23; Conservative 7; Mismatches 19; Indels 5; Gaps 2;

QY 6 WNEGVCTCGTQRRRDTY----LGFQAPVPADQFQHPKPVTVGWAQPC 55
|||||
DB 1 WNCATTCGVTGVRVTCVQLLSFSSVADLPIDKEG-FDASQACVAFQC 53

RESULT 6
/ Sequence 5, Application US/09491522
/ Sequence 5, Application US/09491522
/ GENERAL INFORMATION:
/ APPLICANT: Lapierre, Charles M.
/ APPLICANT: Frodock, Darwin
/ CURRENT FILING DATE: US/09/491,522
/ CURRENT FILING DATE: 1999-09-24
/ NUMBER OF SEQUENCES: 17
/ TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
/ CORRESPONDENCE ADDRESS:
/ STREET: 115 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10013-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: Windows
/ SOFTWARE: FastSeq for Windows Version 2.0b
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/491,522
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/686,133
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Abrams, Samuel B
; REGISTRATION NUMBER: 30,685
; REGISTRATION DATE: 09/08/99
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; FAX: 650-493-5556
; TELEX: 66141 PENNISI
; ADDRESS: 10000 Wilshire Blvd
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; TYPE: 21 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-451-522-5
;
; Query Match 30.8%; Score 106.5; DB 4; Length 1211;
; Best Local Similarity 40.0%; Pred. No. 0.00066;
; Matches 22; Conservative 4; Mismatches 24; Indels 5; Gaps 2;
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 578 MWAPWMSQSVICGRRGTRPVLCT---RTDSDGIGLGE-IRIRATCTGCGC 1028
;
; RESULT 7
; US-09-728-171
; Sequence 171, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; TYPE: PRT
; FILE REFERENCE: P204P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR PUBLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO: 171
; LENGTH: 101
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 50
; DB 1 WYVTSNACRCGCGGRRVTRVTCQKLDAGISTFVNDQMCYQVAPVDFQAG 54
;
; RESULT 8
; US-09-729-173
; Sequence 173, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; TYPE: PRT
; FILE REFERENCE: P204P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR PUBLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO: 173
; LENGTH: 96
;
; Query Match 29.8%; Score 103; DB 4; Length 59;
; Best Local Similarity 40.7%; Pred. No. 2.7e-05;
; Matches 22; Conservative 6; Mismatches 22; Indels 4; Gaps 2;
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 50
; DB 1 WYVTSNACRCGCGGRRVTRVTCQKLDAGISTFVNDQMCYQVAPVDFQAG 54
;
; RESULT 9
; US-09-800-729-217
; Sequence 217, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; TYPE: PRT
; FILE REFERENCE: P204P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2001-03-08
; PRIOR PUBLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO: 217
; LENGTH: 1059
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC-PC 55
; DB 296 MWADSKCTASCGQVRRHVACG-----GSDCGSRPQFTTYAGIPC 343
;
; RESULT 10
; US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 6000977
; GENERAL INFORMATION:
; ORGANISM: Mus musculus
; TYPE: PRT
; FILE REFERENCE: T11a L
; CURRENT APPLICATION NUMBER: US/09/369,364A
; PRIOR APPLICATION NUMBER: PCT/US90/10-30-00
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; PRIOR APPLICATION NUMBER: PCT/US90-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 905
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 852 WYLDWMSCFSTCRGSHRTVEYCDPSQA---STDCBALAFEDAPQCGQC 903
;
; Query Match 29.0%; Score 100.5; DB 4; Length 905;
; Best Local Similarity 33.4%; Pred. No. 0.00097;
; Matches 20; Conservative 5; Mismatches 27; Indels 3; Gaps 1;
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 852 WYLDWMSCFSTCRGSHRTVEYCDPSQA---STDCBALAFEDAPQCGQC 903

```

```

; NAME: Homo sapiens
; REGISTRATION NUMBER: 30,685
; REGISTRATION DATE: 09/08/99
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; FAX: 650-493-5556
; TELEX: 66141 PENNISI
; ADDRESS: 10000 Wilshire Blvd
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; TYPE: 21 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-800-729-217
;
; Query Match 29.3%; Score 101.5; DB 4; Length 56;
; Best Local Similarity 33.3%; Pred. No. 3.8e-05;
; Matches 19; Conservative 7; Mismatches 29; Indels 1; Gaps 1;
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 1 KRVLATCTACGTGQSRKCVARTNKVPEHLCSNGRPANMQRCNTTFC 56
;
; RESULT 9
; US-09-800-729-217
; Sequence 217, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; ORGANISM: Homo sapiens
; TYPE: PRT
; FILE REFERENCE: P204P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIOR APPLICATION NUMBER: PCT/US90/26013
; PRIOR FILING DATE: 2001-03-08
; PRIOR PUBLICATION NUMBER: 60/155,709
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO: 217
; LENGTH: 1059
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC-PC 55
; DB 296 MWADSKCTASCGQVRRHVACG-----GSDCGSRPQFTTYAGIPC 343
;
; RESULT 10
; US-09-369-364A-9
; Sequence 9, Application US/09369364A
; Patent No. 0.00097;
; GENERAL INFORMATION:
; ORGANISM: Mus musculus
; TYPE: PRT
; FILE REFERENCE: T11a L
; CURRENT APPLICATION NUMBER: US/09/369,364A
; PRIOR APPLICATION NUMBER: PCT/US90/10-30-00
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; PRIOR APPLICATION NUMBER: PCT/US90-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 905
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 852 WYLDWMSCFSTCRGSHRTVEYCDPSQA---STDCBALAFEDAPQCGQC 903
;
; Query Match 29.0%; Score 100.5; DB 4; Length 905;
; Best Local Similarity 33.4%; Pred. No. 0.00097;
; Matches 20; Conservative 5; Mismatches 27; Indels 3; Gaps 1;
;
; QY 1 MWVTVWMSVSGDQIGRRRTCTGQAPAFVDFQQLPFPVTRCQAGC 55
; DB 852 WYLDWMSCFSTCRGSHRTVEYCDPSQA---STDCBALAFEDAPQCGQC 903

```

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RESULT 11
US-09-800-729-169
US-09-800-729-169
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: N. et al. 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 60/155,709
NUMBER OF SEQ ID NOS: 60/155,709
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 169
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-169
Query Match 27.6%; Score 95.5; DB 4; Length 58;
Best Local Similarity 34.5%; Pred. No. 0.0002;
Matches 20; Conservative 5; Mismatches 30; Indels 3; Gaps 1;
QY 1 MHVGTWECVSCGGQIGRRDTC--LGPQQAQVPAADFQHLKPVFTVVGNCAGPC 55
DB 1 MLLSDMTCTSCGGTGTGSAICRMKLTGLTVVNSTLCPLPFFSSSRFPQATC 58
RESULT 12
US-09-800-729-124
US-09-800-729-124
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: N. et al. 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 60/155,709
NUMBER OF SEQ ID NOS: 60/155,709
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 124
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-124
Query Match 27.6%; Score 95.5; DB 4; Length 54;
Best Local Similarity 34.5%; Pred. No. 0.0021;
Matches 20; Conservative 5; Mismatches 30; Indels 3; Gaps 1;
QY 1 MHVGTWECVSCGGQIGRRDTC--LGPQQAQVPAADFQHLKPVFTVVGNCAGPC 55
DB 83 MLLSDMTCTSCGGTGTGSAICRMKLTGLTVVNSTLCPLPFFSSSRFPQATC 140
RESULT 13
US-09-800-729-167
US-09-800-729-167
Patent No. 6605592
GENERAL INFORMATION:
APPLICANT: N. et al. 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 60/155,709
NUMBER OF SEQ ID NOS: 60/155,709
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-167
Query Match 27.6%; Score 95.5; DB 4; Length 54;
Best Local Similarity 34.5%; Pred. No. 0.0021;
Matches 20; Conservative 5; Mismatches 30; Indels 3; Gaps 1;
QY 1 MHVGTWECVSCGGQIGRRDTC--LGPQQAQVPAADFQHLKPVFTVVGNCAGPC 55
DB 83 MLLSDMTCTSCGGTGTGSAICRMKLTGLTVVNSTLCPLPFFSSSRFPQATC 140

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; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/09/800,729
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patent in Ver. 2.0
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-167
Query Match 27.5%; Score 95; DB 4; Length 60;
Best Local Similarity 30.9%; Pred. No. 0.0024;
Matches 21; Conservative 5; Mismatches 10; Indels 3; Gaps 3;
QY 1 MHVGTWECVSCGGQIGRRDTCGCGQAQVPAADFQHL-----P 42
DB 1 MEIQMSPSITGVHGLTIDV-----FCHLLSRNMTVILADELCROP 46
QY 43 KPTVTRGC 50
DB 47 KPTVTRGC 54
RESULT 14
US-09-930-872-4
US-09-930-872-4
Sequence 4; Application US/09330872
Patent No. 6448388
APPLICANT: Hilbus, Erin
APPLICANT: Fiddle, Carl Johan
TITLE OF INVENTION: NO. 6448388 Human Proteases and Polynucleotides Encoding the
CURRENT APPLICATION NUMBER: US/09330872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1224
TYPE: PRT
ORGANISM: homo sapiens
US-09-930-872-4
Query Match 27.0%; Score 93.5; DB 4; Length 1224;
Best Local Similarity 36.2%; Pred. No. 0.0089;
Matches 21; Conservative 5; Mismatches 29; Indels 3; Gaps 2;
QY 1 MHVGTWECVSCGGQIGRRDTC--LGPQQAQVPAADFQHLKPVFTVVGNCAGPC 55
DB 930 WNSPFWACSTCGHGRASNAKASINVSQAQLDPATCTEYRMEACLRG 1047
RESULT 15
US-09-930-872-4
US-09-930-872-4
Sequence 4; Application US/08919914
Patent No. 5876963
GENERAL INFORMATION:
APPLICANT: Hutchinson, Peter
APPLICANT: Hutchinson, Nancy
APPLICANT: Lawton, Michael
APPLICANT: Mesma, Holly
APPLICANT: Mesma, Lynn E.
APPLICANT: NURY, David
TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHATASE
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION NUMBER: 5876963
ADDRESS: Enovate Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

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1  ZIP: 94304
2  COMPUTER: IBM COMPATIBLE FROM:
3  MEDIUM TYPE: Diskette
4  COMPUTER: IBM Compatible
5  OPERATING SYSTEM: DOS
6  CURRENT APPLICATION DATA: Windows Version 2.0
7  APPLICATION NUMBER: US/08/918.914
8  FILING DATE: Filed Herewith
9  PRIOR APPLICATION DATA:
10 APPLICATION NUMBER:
11 FILING DATE:
12 ATTORNEY/AGENT INFORMATION:
13 NAME/REGISTRATION NUMBER: 36,749
14 REFERENCE/DOCKET NUMBER: PF-0369
15 TELEPHONE: 415-845-0555
16 TELEFAX: 415-845-4166
17 TELEX:
18 INFORMATION FOR US: 4:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 788 amino acids
21 TYPE: amino acid
22 TOPOLOGY: single
23 IMMEDIATE SOURCE:
24 LIBRARY: Genbank
25 CDS: 1070094
26 US-08-918-914-4
27
28 Query Match: 26.94; Score 93; DB 2; Length 788;
29 Identical Similarity: 100%; Positives: 100%;
30 Matches 22; Conservative: 4; Mismatches 15; Indels 12; Gaps 3;
31
32 Oy 6 WMECSYSGIGQRRTQLGPOQAAPVADFQHL---DEPTVYDCAQPC 55
33 Db 560 WQCSYSGYGVAVFTLLG-----GVFSDHLQCPK-TEBACQCP 603
34
35 Search completed: March 13, 2004, 07:46:08
36 Job time : 2.4468 secs

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